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GenCore version 5.1.6

protein - protein search, using sw model

on: January 7, 2005, 10:01:57 ; Search time 86 Seconds
(without alignments)

50.055 Million cell updates/sec

e: US-09-699-224A-1

Exact score: 63

Tolerance: 1 PVIDBNGLFPAP 12

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Matched: 2002273 seqs, 358729299 residues

Query Match 100.0%; Score 63; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX DT 20-NOV-2003 (first entry)

Acinetobacter baumannii protein #2392.

Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
 plant biocontrol agent.

RESULT 2
 AAB97125
 ID AAB97125 standard; peptide; 15 AA.
 XX
 AC AAB97125;
 XX DT 07-AUG-2001 (first entry)
 DE Conserved gonococcal mAb 2C7 epitope mimic fusion peptide.
 XX
 KW Peptide mimic; vaccine; gonococcal; epitope; Neisseria gonorrhoeae;
 infection; monoclonal antibody 2C7; mAb 2C7; fusion.
 XX OS Synthetic.
 XX PR 29-OCT-1999; 99US-0162491P.
 XX PN WO200132692-A2.
 XX PD 10-MAY-2001.
 XX PF 27-OCT-2000; 2000WO-US029749.
 XX PR 29-OCT-1999; 99US-0162491P.
 XX PA (RICE P A. - RICE P A.
 PA (NGAMPAUTADOL J.
 PA (GULATI S.
 XX PI Rice PA, Ngampabutadol J, Gulati S;
 XX DR WPI: 2001-343473/36.
 XX PT New peptide mimics of conserved gonococcal epitopes not present in human blood group antigens, useful for prophylaxis of Neisseria gonorrhoeae infections.
 XX PS Claim 23; Fig 2; 57pp; English.
 XX The invention relates to novel peptide mimics of conserved gonococcal epitopes which are not present in human blood group antigens. The peptide mimics are useful for immunising against Neisseria gonorrhoeae infections. The present sequence is a peptide mimic which binds to an epitope of the Neisseria gonorrhoeae monoclonal antibody 2C7. Peptides were synthesised by random peptide display and were subjected to five rounds of positive selection with mAb 2C7 to identify those able to bind mAb 2C7. Two cysteine flanking regions were added to the N- and C-termini of a peptide mimic produced by this method to generate the present sequence, which is also an effective peptide mimic of the mAb 2C7 epitope
 XX SQ Sequence 15 AA;
 XX AC AAV74789;
 XX DT 21-MAR-2000 (first entry)

Neisseria meningitidis ORF 261 protein sequence SEQ ID NO:1052.

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 antigenic; diagnosis; immunogenic; infection; meningitis; septicæmia;
 antibacterial; gene therapy.

RESULT 3
 ADA5231
 ID ADA5231 standard; protein; 64 AA.
 XX OS Neisseria meningitidis.
 XX PN WO9957280-A2.
 XX PD 11-NOV-1999.
 AC ADA35231;

PF 30-APR-1999; 99WO-US009346.
 XX PR 01-MAY-1998; 98US-0083758P.
 PR 01-MAY-1998; 98US-0094169P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-009900P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 09-OCT-1998; 98US-0103799P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX PI Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
 PI Petersen J, Pizza M, Rappuoli R, Ratti G, Scarselli M;
 PI Tettelin H, Venter JC;
 XX DR WPI; 2000-062150/05.
 DR N-PSDB; AAZ53551.
 XX PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX PS Claim 2; Page 604; 1453PP; English.
 XX CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ55473 represent PCR primers used in the exemplification of the present invention. The PCR primers used in the exemplification of the present invention. The CC polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture CC of medicaments for treating or preventing infection due to Neisseria bacteria (e.g. meningitis and septicæmia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
 XX SQ Sequence 232 AA;
 XX Query Match 65.1%; Score 41; DB 3; Length 232;
 Best Local Similarity 64.3%; Pred. No. 41;
 Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 Qy 1 IPVLDENGU--FAP 12
 Db 194 LPVLESNGLDVFAP 207
 RESULT 6
 ABU19644
 ID ABU19644 standard; protein; 691 AA.
 XX AC ABU19644;
 XX DT 19-JUN-2003 (first entry)
 XX DB Protein encoded by Prokaryotic essential gene #5171.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Borrelia cepacia.
 XX PN WO20027183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 XX PR 06-SEP-2001; 2001US-00948993.
 XX PR 25-OCT-2001; 2001US-0342923P.
 XX PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX PN WO200277183-A2.
 PR XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX PD 03-OCT-2002.
 DR WPI: 2003-029926/02.
 DR XX 21-MAR-2002; 2002WO-US009107.
 N-PSDB; ACR23514.
 XX PR 21-MAR-2001; 2001US-00815242.
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX PR 06-SEP-2001; 2001US-00948993.
 PT 25-OCT-2001; 2001US-0312923P.
 PR 08-DEC-2002; 2002US-0072851.
 PR 06-MAR-2002; 2002US-0362699P.
 PT XX (ELIT-) ELITRA PHARM INC.
 PA
 PS Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 N-PSDB; ACA26863.
 CC New antisense nucleic acids, useful for identifying proteins or screening
 CC for homologous nucleic acids required for cellular proliferation to
 CC isolate candidate molecules for rational drug discovery programs.
 XX PA
 PS Claim 25; SEQ ID NO 50917; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 691 AA;
 SQ Query Match 65.1%; Score 41; DB 6; Length 691;
 Best Local Similarity 88.9%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPVLDENG1L 9
 Db 674 IPVLDENG1L 682
 SQ Sequence 696 AA;
 SQ Query Match 65.1%; Score 41; DB 6; Length 696;
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 AC ABU22993;
 AC ABU22993;
 XX DT 19-JUN-2003 (first entry)
 DB Protein encoded by Prokaryotic essential gene #8520.
 XX RESULT 8
 ID ABR42508 standard; protein; 702 AA.
 OS Bordetella pertussis.

PI	L'maisonneuve J, Zhang Y, Jen S, Carter D;	DR	N-PSDB; ACF64431.
XX	WPI; 2001-616774/71.	DR	N-PSDB; AA559582.
DR		XX	
Propionibacterium acnes	Polypeptides and nucleic acids useful for	PT	Propionibacterium acnes polypeptides and polymucleotides encoding the
PT	vaccinating against and diagnosing infections, especially useful for	PT	polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT	treating acne vulgaris.	PT	or for stimulating an immune response specific for a P. acnes protein.
XX		XX	
PS	Example 1; SEQ ID NO 18525; 1481pp; English.	PS	Example 1; SEQ ID NO 18525; 1069pp; English.
XX		XX	
CC	Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic	CC	The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC	polypeptides. The proteins and their associated DNA sequences are used in	CC	encoding a Propionibacterium acnes protein. The invention also relates to
CC	the treatment, prevention and diagnosis of medical conditions caused by	CC	polypeptides encoded by the polynucleotides (ABM3624-ABM64536) and to
CC	P. acnes. The disorders include SAPHO syndrome (synovitis, acne,	CC	immunogenic fragments of P. acnes polypeptides. The invention
CC	pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis,	CC	additionally encompasses expression vectors and host cells comprising a
CC	P. acnes is also involved in infections of bone, joints and the central	CC	polynucleotide of the invention; antibodies against polypeptides of the
CC	nervous system, however it is particularly involved in the inflammatory	CC	invention; fusion proteins comprising a polypeptide of the invention; a
CC	lesions associated with acne vulgaris. A method for detecting the	CC	method for stimulating an immune response specific for a P. acnes
CC	presence or absence of P. acnes in a patient comprises contacting a	CC	polypeptide and an isolated T cell population comprising T cells prepared
CC	sample with a binding agent that binds to the proteins of the invention	CC	via this method; a vaccine composition comprising P. acnes polypeptides,
CC	and determining the amount of bound protein in the sample. The	CC	polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the
CC	polypeptides may be used as antigens in the production of antibodies	CC	polypeptides are useful for diagnosing, preventing or treating acne
CC	specific for P. acnes proteins. These antibodies can be used to	CC	vulgaris, or for stimulating an immune response specific for a P. acnes
CC	downregulate expression and activity of P. acnes polypeptides and	CC	protein. The polynucleotides can also be used as probes or primers for
CC	therefore treat P. acnes infections. The antibodies may also be used as	CC	nucleic acid hybridisation. The vaccine composition is useful for the
CC	diagnostic agents for determining P. acnes presence, for example, by	CC	stimulation of an immune response against P. acnes, or for treating acne,
CC	enzyme linked immunosorbent assay (ELISA). Note: The sequence data for	CC	this kit is useful for performing a diagnostic assay. The present
CC	this patent did not form part of the printed specification, but was	CC	sequence represents a polypeptide predicted to be encoded by an ORF (open
CC	obtained in electronic format directly from WIPO at	CC	reading frame) contained within the P. acnes polynucleotides of the
CC	ftp.wipo.int/pub/published_pct_sequences	CC	invention. Note: The sequence data for this patent did not form part of
SQ	Sequence 724 AA;	SQ	the printed specification, but was obtained in electronic format directly
Query Match	Score 41; DB 4; Length 724;	Query Match	65.1%; Score 41; DB 6; Length 724;
Best Local Similarity	Pred. No. 1.6e+02;	Best Local Similarity	58.3%; Pred. No. 1.6e+02;
Matches	2; Mismatches 3; Indels 0;	Matches	2; Mismatches 3; Indels 0;
Db	309 VPMDDENGMTTP 320	Db	Gaps 0;
Qy	1 IPVLDENGTLFAP 12	Qy	1 IPVLDENGTLFAP 12
	: :		: :
XX		Db	309 VPMDDENGMTTP 320
RESULT 11		RESULT 12	
ID	ABM53849 standard; protein; 724 AA.	ID	ABB61313 standard; protein; 224 AA.
XX		XX	
AC	ABM53849;	AC	ABB61313;
XX		XX	
DT	20-OCT-2003 (first entry)	DT	26-MAR-2002 (first entry)
XX		XX	
DB	Propionibacterium acnes predicted ORF-encoded polypeptide #18525.	DB	Drosophila melanogaster polypeptide SEQ ID NO 10731.
XX		XX	
KW	Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;	KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	immuno-modulant; immune response; vaccine.	KW	pharmaceutical.
XX		XX	
OS	Propionibacterium acnes.	OS	WIPO200171042-A2.
XX		XX	
PN	WO2003033515-A1.	PN	27-SEP-2001.
XX		XX	
PR	15-OCT-2001; 2001US-00978825.	PR	23-MAR-2001; 2001WO-US009231.
XX		XX	
(CORI-) CORIXA CORP.		(CORI-) CORIXA CORP.	
XX		XX	
PI	Mitcham JL, Skeiky YAW, Persing DH, Bhatria A, Maisonneuve JL;	PI	23-MAR-2000; 2000US-0191637P.
PI	Zhang Y, Wang S, Jen S, Jones MJ, Benson DR, Carter D;	PR	11-JUL-2000; 2000US-00614150.
PI	Bartch B, Valiee-Douglas J,	XX	(PEKE) PE CORP NY.
XX		PA	
WPI;	2003-381789/36.	XX	

PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL0516.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX Disclosure: SEQ ID NO 10731; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-AB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 224 AA;

Query Match	63.5%	Score 40;	DB 4;	Length 224;
Best Local Similarity	60.0%;	Pred. No.	60;	
Matches	6;	Conservative	3;	Mismatches 1;
Qy	1 IPVLDENGILP 10			Indels 0;
Db	: : :			Gaps 0;
	57 VPMDDNGTFF 66			

RESULT 13
 ABM68527
 ID ABM68527 standard; protein; 400 AA.
 XX AC ABM68527;
 XX DT 20-NOV-2003 (first entry)
 XX DE Photorhabdus luminescens protein sequence #1624.
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough.

XX OS Photorhabdus luminescens.

XX PN WO200294867-A2.

XX PD 28-NOV-2002.

XX PF 07-FEB-2002; 2002WO-IB003040.

XX PR 07-FEB-2001; 2001FR-00001659.

PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;

XX DR WPI; 2003-148459/14.

XX PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX PS Claim 2; SEQ ID NO 1624; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded
 CC proteins from Photorhabdus luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of *P. luminescens* and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of *P. luminescens*, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than *P. luminescens* and are able to alter response or sensitivity to toxins and antibiotics produced by *P. luminescens*. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibiotics useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which *P. luminescens* is a model (particularly plague and whooping cough). This sequence represents one of the isolated *P. luminescens* proteins

SQ Sequence 400 AA;

Query Match	63.5%	Score 40;	DB 6;	Length 400;
Best Local Similarity	50.0%;	Pred. No.	1.2e+02;	
Matches	6;	Conservative	4;	Mismatches 2;
Qy	1 IPVLDENGILP 12			Indels 0;
Db	: : :			Gaps 0;
	12 LPATDNGINAP 23			

RESULT 14
 ADA36467
 ID ADA36467 standard; protein; 441 AA.
 XX AC ADA36467;
 XX DT 20-NOV-2003 (first entry)
 XX DE Acinetobacter baumannii protein #3628.

XX KW Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
 KW plant biocontrol agent.

XX DB Acinetobacter baumannii.

XX OS Acinetobacter baumannii.

XX PN US562958-B1.

XX PD 13-MAY-2003.

XX PP 04-JUN-1999;

XX PR 09-JUN-1998;

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Bretton G, Bush D;

XX DR WPI; 2003-576092/54.

XX DR N-PSDB; ADA36467.

XX PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.

XX PS Example; SEQ ID NO 7754; 328pp; English.

CC The invention relates to isolated *Acinetobacter baumannii* nucleic acids. The *A. baumannii* nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of *A. baumannii* and other *Acinetobacter* species in a sample, in screening

or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissue, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

SQ Sequence 92 AA;
 Query Match Score 39; DB 4; Length 92;
 Best Local Similarity 63.6%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PVDENGLPAP 12
 Db 46 PLLOETGAFAP 56

RESULT 17
 AAG56366 Standard; protein; 93 AA.
 AC AAG56366;
 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 72444.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PP 25-FEB-2000; 2000EP-00301439.
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-012180P.
 PR 09-MAR-1999; 99US-0121548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 19-APR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0128845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 06-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 07-MAY-1999; 99US-0132487P.
 PR 11-MAY-1999; 99US-01324863P.
 PR 14-MAY-1999; 99US-0132418P.
 PR 14-MAY-1999; 99US-0132419P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135153P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 28-MAY-1999; 99US-0136392P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 10-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
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 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-013763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0143390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0141977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 19-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 21-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P. PR 21-JUL-1999; 99US-0145088P. PR 22-JUL-1999; 99US-0145085P. PR 22-JUL-1999; 99US-0145087P. PR 22-JUL-1999; 99US-0145089P. PR 22-JUL-1999; 99US-0145122P. PR 23-JUL-1999; 99US-0145145P. PR 23-JUL-1999; 99US-0145218P. PR 23-JUL-1999; 99US-0145224P. PR 24-AUG-1999; 99US-014526P. PR 26-JUL-1999; 99US-0145276P. PR 27-JUL-1999; 99US-0145931P. PR 27-JUL-1999; 99US-0145938P. PR 27-JUL-1999; 99US-0145948P. PR 27-JUL-1999; 99US-0145919P. PR 28-JUL-1999; 99US-0145951P. PR 02-AUG-1999; 99US-0146316P. PR 02-AUG-1999; 99US-0146388P. PR 02-AUG-1999; 99US-0146389P. PR 03-AUG-1999; 99US-0147038P. PR 04-AUG-1999; 99US-0147204P. PR 04-AUG-1999; 99US-0147302P. PR 05-AUG-1999; 99US-0147192P. PR 06-AUG-1999; 99US-0147260P. PR 06-AUG-1999; 99US-0147503P. PR 06-AUG-1999; 99US-0147416P. PR 09-AUG-1999; 99US-0147935P. PR 10-AUG-1999; 99US-0148171P. PR 11-AUG-1999; 99US-0148319P. PR 12-AUG-1999; 99US-0148341P. PR 13-AUG-1999; 99US-0148365P. PR 13-AUG-1999; 99US-0148384P. PR 16-AUG-1999; 99US-0149168P. PR 17-AUG-1999; 99US-0149175P. PR 18-AUG-1999; 99US-0149426P. PR 20-AUG-1999; 99US-0149722P. PR 20-AUG-1999; 99US-0149723P. PR 20-AUG-1999; 99US-0149729P. PR 23-AUG-1999; 99US-0149902P. PR 23-AUG-1999; 99US-0149930P. PR 25-AUG-1999; 99US-0150566P. PR 26-AUG-1999; 99US-0150584P. PR 27-AUG-1999; 99US-0151065P. PR 27-AUG-1999; 99US-0151066P. PR 27-AUG-1999; 99US-0151080P. PR 30-AUG-1999; 99US-0151303P. PR 31-AUG-1999; 99US-0151438P. PR 01-SEP-1999; 99US-01515130P. PR 07-SEP-1999; 99US-01523363P. PR 10-SEP-1999; 99US-0152070P. PR 13-SEP-1999; 99US-0153758P. PR 15-SEP-1999; 99US-0154018P. PR 16-SEP-1999; 99US-0154039P. PR 20-SEP-1999; 99US-0154779P. PR 23-SEP-1999; 99US-0155139P. PR 24-SEP-1999; 99US-0155486P. PR 28-SEP-1999; 99US-0156458P. PR 29-SEP-1999; 99US-0156596P. PR 04-OCT-1999; 99US-0157117P. PR 05-OCT-1999; 99US-0157753P. PR 06-OCT-1999; 99US-0157865P. PR 07-OCT-1999; 99US-015829P. PR 14-OCT-1999; 99US-0158232P. PR 12-OCT-1999; 99US-0158369P. PR 13-OCT-1999; 99US-0159293P. PR 13-OCT-1999; 99US-0159295P. PR 14-OCT-1999; 99US-0159295P. PR 14-OCT-1999; 99US-0159329P. PR 14-OCT-1999; 99US-0159330P. PR 14-OCT-1999; 99US-0159637P. PR 14-OCT-1999; 99US-0159638P. PR 18-OCT-1999; 99US-0159584P.

PR 21-OCT-1999; 99US-0160741P. PR 21-OCT-1999; 99US-0160767P. PR 21-OCT-1999; 99US-0160768P. PR 21-OCT-1999; 99US-0160770P. PR 21-OCT-1999; 99US-0160844P. PR 21-OCT-1999; 99US-0160845P. PR 22-OCT-1999; 99US-0160980P. PR 22-OCT-1999; 99US-0160981P. PR 22-OCT-1999; 99US-0160989P. PR 25-OCT-1999; 99US-0161404P. PR 25-OCT-1999; 99US-0161405P. PR 25-OCT-1999; 99US-0161466P. PR 26-OCT-1999; 99US-0161339P. PR 26-OCT-1999; 99US-0161360P. PR 26-OCT-1999; 99US-0161361P. PR 28-OCT-1999; 99US-0161930P. PR 28-OCT-1999; 99US-0161932P. PR 28-OCT-1999; 99US-0161933P. PR 29-OCT-1999; 99US-0162121P. PR 29-OCT-1999; 99US-0162122P.

Query Match Score 39; DB 3; Length 93; Best Local Similarity 45.5%; Pred. No. 33; Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Query 1 IPVLDENGLFA 11
Matches :|:||:|:
Db 44 LPIYEENGIFTS 54

RESULT 18
ID AAG56365 standard; protein; 100 AA.
XX
AC AAG56365;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 72443.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FBB-2000; 2000EP-00301439.
XX PR 25-FBB-1999; 99US-0121815P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-012518P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127412P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-012845P.
PR 19-APR-1999; 99US-013007P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132448P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132466P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-012863P.

PR	11-MAY-1999;	99US-0134256B.	99US-0145218P.
PR	14-MAY-1999;	99US-0134218P.	99US-0145224P.
PR	14-MAY-1999;	99US-0134219P.	99US-0145216P.
PR	14-MAY-1999;	99US-0134221P.	99US-014513P.
PR	14-MAY-1999;	99US-0134370B.	99US-014518P.
PR	18-MAY-1999;	99US-0134768P.	99US-014519P.
PR	19-MAY-1999;	99US-0134941P.	99US-014511P.
PR	20-MAY-1999;	99US-0135124P.	99US-0146386P.
PR	21-MAY-1999;	99US-0135353D.	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	99US-0147038P.
PR	27-MAY-1999;	99US-0136392D.	99US-0147204P.
PR	01-JUN-1999;	99US-0136782D.	99US-0147302P.
PR	03-JUN-1999;	99US-0137222B.	99US-0147260P.
PR	04-JUN-1999;	99US-0137528D.	99US-0147261P.
PR	07-JUN-1999;	99US-0137724P.	99US-0147310P.
PR	08-JUN-1999;	99US-0138094P.	99US-0147311P.
PR	10-JUN-1999;	99US-0138540B.	99US-014735P.
PR	10-JUN-1999;	99US-0138847P.	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	99US-0148318P.
PR	16-JUN-1999;	99US-0139452P.	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	99US-0147491P.
PR	18-JUN-1999;	99US-0139454P.	99US-0148684P.
PR	18-JUN-1999;	99US-0139455P.	99US-0149368P.
PR	18-JUN-1999;	99US-0139461P.	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	99US-0149723P.
PR	18-JUN-1999;	99US-0139492P.	99US-014929P.
PR	22-JUN-1999;	99US-0139559P.	99US-014902P.
PR	22-JUN-1999;	99US-0139460P.	99US-014930P.
PR	22-JUN-1999;	99US-0139461P.	99US-0150566P.
PR	23-JUN-1999;	99US-0139462P.	99US-0150884P.
PR	18-JUN-1999;	99US-0139463P.	99US-0151065P.
PR	18-JUN-1999;	99US-0139750P.	99US-0151066P.
PR	18-JUN-1999;	99US-0139763P.	99US-0151080P.
PR	28-JUN-1999;	99US-0140695P.	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	99US-0153175P.
PR	30-JUN-1999;	99US-0141287P.	99US-0154018P.
PR	01-JUL-1999;	99US-0140353P.	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	99US-0155179P.
PR	02-JUL-1999;	99US-0142055P.	99US-0155363P.
PR	06-JUL-1999;	99US-0142050P.	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	99US-0156458P.
PR	16-JUL-1999;	99US-0144086P.	99US-0156596P.
PR	12-JUL-1999;	99US-0142977P.	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	99US-0157117P.
PR	14-JUL-1999;	99US-0142055P.	99US-0157753P.
PR	15-JUL-1999;	99US-0144332P.	99US-0157865P.
PR	19-JUL-1999;	99US-0144334P.	99US-0158232P.
PR	19-JUL-1999;	99US-0144085P.	99US-0159330P.
PR	16-JUL-1999;	99US-01442920P.	99US-0159331P.
PR	19-JUL-1999;	99US-0144335P.	99US-0159331P.
PR	20-JUL-1999;	99US-014452P.	99US-0159637P.
PR	19-JUL-1999;	99US-0144331P.	99US-0159638P.
PR	20-JUL-1999;	99US-0144332P.	99US-0159295P.
PR	19-JUL-1999;	99US-0144333P.	99US-0159295P.
PR	21-JUL-1999;	99US-0144814P.	99US-0160741P.
PR	21-JUL-1999;	99US-0145086P.	99US-0160767P.
PR	22-JUL-1999;	99US-0145088P.	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	99US-0160980P.

PR	22-OCT-1999;	99US-0160981P.	DR	N-PSDB; AAD13379.
PR	22-OCT-1999;	99US-0160989P.	XX	New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders.
PR	25-OCT-1999;	99US-016104P.	PT	
PR	25-OCT-1999;	99US-016105P.	PT	
PR	25-OCT-1999;	99US-016105P.	XX	
PR	25-OCT-1999;	99US-0161406P.	XX	
PR	26-OCT-1999;	99US-016159P.	PS	Claim 11; Page 521; 558pp; English.
PR	26-OCT-1999;	99US-016160P.	XX	
PR	26-OCT-1999;	99US-016161P.	CC	AAD13345-AAD1401 represent cDNAs corresponding to 22 human secreted protein genes, and AAE07051-AAE07105 represent the proteins they encode.
PR	28-OCT-1999;	99US-016190P.	CC	The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.
PR	28-OCT-1999;	99US-016192P.	CC	Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin diseases (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, and infections. The
PR	28-OCT-1999;	99US-016193P.	CC	proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention
PR	29-OCT-1999;	99US-016242P.	CC	XX
Query Match	61.9%;	Score 39; DB 3; Length 100;	Query Match	61.9%; Score 39; DB 4; Length 135;
Best Local Similarity	45.5%;	Pred. No. 36;	Best Local Similarity	63.6%; Pred. No. 51;
Matches	5;	Mismatches 1; Indels 0;	Mismatches	1; Gaps 0;
Qy	1 IPVLDENGFLA 11		Qy	2 PVLDEGLPAP 12
	: : : : : :			: : : : :
Db	51 LPYEEENGIFS 61			46 PLLQETGAP 56
RESULT 19			Db	
AAE07085			RESULT 20	
ID	AAE07085 standard; protein; 135 AA.		AAE07058	
XX			ID	AAE07058 standard; protein; 135 AA.
AC	AAE07085;		XX	
XX			AC	AAE07058;
DT	16-OCT-2001 (first entry)		XX	
XX			DT	16-OCT-2001 (first entry)
DB	Human gene 8 encoded secreted protein HHTLB76, SEQ ID NO:102.		DB	Human gene 8 encoded secreted protein HHTLB76, SEQ ID NO:75.
XX			XX	
XX	Human secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerability; cell culture; chemotaxis; food additive; gene therapy; binding partner identification.		XX	Human secreted protein, proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerability; cell culture; chemotaxis; food additive; gene therapy; binding partner identification.
OS	Homo sapiens.		XX	
XX			XX	
FH	Key	Location/Qualifiers	XX	
FT	Peptide	1 ..24	XX	
FT		/label= Signal_peptide	XX	
FT	Protein	25 ..135	XX	
FT		/label= Mature_human_secreted_protein	XX	
FT	Misc-difference	125	XX	
FT		/label= Unknown	XX	
FT		/note= "Encoded by GYG"	XX	
NN	W0200154708-A1.		XX	
XX	02-AUG-2001.		XX	
PD	17-JAN-2001; 2001WO-US001434.		XX	
PR	31-JAN-2000; 2000US-0179065P.		KW	
PR	04-FEB-2000; 2000US-0180628P.		KW	
PR	18-AUG-2000; 2000US-0226279P.		KW	
PR	05-DEC-2000; 2000US-0251988P.		KW	
PR	05-JAN-2001; 2001US-0259678P.		KW	
XX	(HUNA-) HUMAN GENOME SCI INC.		KW	
XX	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Shi Y, Choi GH; Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Barash SC;		OS	
PI	Fischella M, Ni J, Ruben SM,		XX	
XX	Barash SC;		PH	Location/Qualifiers
DR	WPI; 2001-488743/53.		FT	1 ..24
			FT	/label= Signal_peptide

FT	Protein	25..135	AC	ABB61361;
XX		/label= Mature_human_secreted_protein	XX	26-MAR-2002 (first entry)
PN	WO200154708-A1.		DT	
XX	02-AUG-2001.		DE	Drosophila melanogaster polypeptide SEQ ID NO 10875.
PD	17-JAN-2001; 2001WO-US001434.		XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX	31-JAN-2000; 200003-0179065P.		KW	Drosophila; melanogaster.
PR	04-FEB-2000; 200003-0180628P.		XX	
PR	18-AUG-2000; 200003-0226279P.		PN	WO200171042-A2.
PR	05-JAN-2001; 200003-0251988P.		XX	
PR	05-JAN-2001; 200010S-0259678P.		PD	27-SEP-2001.
XX	(HUMAN) HUMAN GENOME SCI INC.		XX	
XX	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR,		XX	23-MAR-2001; 2001WO-US009231.
PI	Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH,		PR	20000US-0191637P.
PI	Fiscella M, Ni J, Ruben SM, Barash SC,		PR	11-JUL-2000; 20000US-00614150.
XX	DR WPI; 2001-488743/53.		XX	
PT	PT New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders.		PA	(PEKE) PE CORP NY.
XX	DR N-PSDB; AAD13352.		XX	
XX	Claim 11; Page 494; 558pp; English.		PI	Venter JC, Adams M, Li PW, Myers EW;
CC	AAD13345-AAD11401 represent cDNAs corresponding to 22 human secreted protein genes, and AAE07129 represent the proteins they encode.		XX	
CC	AAE07106-AAE07129 represent human secreted protein fragments or variants.		PS	Disclosure; SEQ ID NO 10875; 21pp + Sequence Listing; English.
CC	The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.		XX	
CC	Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angogenic disorders, kidney disorders, gastrointestinal disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chromatography, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention		PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX	Sequence 135 AA;		XX	
SQ	Query Match Best Local Similarity 61.9%; Score 39; DB 4; Length 135; Matches 63.6%; Pred. No. 51; Mismatches 1; Indels 3; Gaps 0;		XX	Query Match Best Local Similarity 61.9%; Score 39; DB 4; Length 225; Matches 7; Pred. No. 93; Mismatches 1; Indels 0; Gaps 0;
Qy	2 FVLDENGFLFAP 12		Qy	1 IPVDENG 8
Db	:		Db	56 IPVDENG 63
XX	Sequence 135 AA;		RESULT 22	
SQ			ID	AAG52033
Qy			ID	AAG52033 standard; protein; 316 AA.
Db			XX	
XX			XX	
Qy			AC	AAG52033;
Db			XX	
XX			DT	26-SEP-2001 (first entry)
Qy			XX	C glutamicum protein fragment SEQ ID NO: 5787.
Db			XX	Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
XX			KW	
XX			OS	Corynebacterium glutamicum.
XX			XX	
XX			PN	EP1108790-A2.
XX			XX	20-JUN-2001.
XX			PD	

RESULT 21
ABB61361
ID ABB61361 standard; protein; 225 AA.
XX

XX Novel barnacle kipris larva-specific adhesion/metamorphosis-related gene
 PF useful for identifying inhibitors of barnacle adhesion.
 XX
 XX
 PR 18-DEC-2000; 2000EP-00127688.
 PR 16-DEC-1999; 99EP-00377484.
 PR 07-APR-2000; 2000EP-00159162.
 PR 03-AUG-2000; 2000EP-00280988.
 PA (KYOWA) KYOWA HAKKO KOGYO KK.
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi M,
 Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX DR WPI; 2001-376931/40.
 DR N-PSDB; AAH67252.
 XX DR N-PSDB; AAH67252.
 PR Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
 PR SEQ ID NO 5787; 246pp + Sequence Listing; English.
 CC The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
 SQ Sequence 316 AA;
 Query Match 61.9%; Score 39; DB 4; Length 316;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 LDENGIFAP 12
 Db 167 VDENGKFP 175
 XX DR 02-FEB-2001 (first entry)
 XX DE AAB23269 standard; protein; 676 AA.
 XX AC AAB23269;
 XX DT 02-FEB-2001 (first entry)
 XX DE Balanus amphitrite adhesion/metamorphosis-related protein Bcs-3.
 XX PN JP20000228985-A.
 XX PD 22-AUG-2000.
 XX OS Balanus amphitrite.
 XX PN JP20000228985-A.
 XX PR 09-FEB-1999; 99JP-00031067.
 XX PR 09-FEB-1999; 99JP-00031067.
 PA (KAIYO) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 DR WPI; 2000-649634/63.
 DR N-PSDB; AAA97603.

XX PT
 PT
 XX PS
 XX
 XX
 CC The invention relates to six larva-specific adhesion/metamorphosis-related genes from the barnacle *Balanus amphitrite* (cDNAs given in AAA97601-A97606) and to the proteins they encode (AA23267-B23272). The genes and the proteins can be used for screening for a substance that inhibits the adhesion or metamorphosis of barnacle larvae, which may be useful in antifouling compositions for use in the shipping industry. The present sequence represents the *Balanus amphitrite* adhesion/metamorphosis-related protein Bcs-3
 XX SQ Sequence 676 AA;
 Query Match 61.9%; Score 39; DB 3; Length 676;
 Best Local Similarity 87.5%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 DENGIFAP 12
 Db 563 DENGIFLP 570
 XX DR 02-FEB-2001 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #6846.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX AC ABU21319;
 XX DT 19-JUN-2003 (first entry)
 XX DE ABU21319 standard; protein; 688 AA.
 XX ID ABU21319
 XX AC ABU21319;
 XX DT 19-JUN-2003 (first entry)
 XX DE DE
 XX KW Burkholderia fungorum.
 XX OS WO200277183-A2.
 XX PN 03-OCT-2002.
 XX PD 21-MAR-2002; 2002WO-US009107.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PR 21-MAR-2001; 2001US-06815242.
 XX PR 06-SEP-2001; 2001US-00948933.
 XX PR 25-OCT-2001; 2001US-034923P.
 XX PR 08-FEB-2002; 2002US-00072851.
 XX PR 06-MAR-2002; 2002US-0362693P.
 XX PA DR 2003-029926/02.
 XX DR N-PSDB; AC25189.
 XX PS Claim 25; SEQ ID NO 49243; 176pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product; or (8) that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (9)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which the test compound that inhibits proliferation of an
 CC organism acts; (10) manufacturing an antibiotic; (11) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct Sequences

SQ Sequence 688 AA;

Query Match 61.9%; Score 39; DB 6; Length 688;
 Best Local Similarity 77.8%; Pred. No. 3.5e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENG1L 9
 Db 672 IPVLDENG1M 680

RESULT 25
 ID AAW98828 standard; protein; 2893 AA.

Qy 1 IPVLDENG1L 9
 Db 672 IPVLDENG1M 680

RESULT 25
 ID AAW98828 standard; protein; 2893 AA.

Qy 1 IPVLDENG1L 9
 Db 672 IPVLDENG1M 680

Query Match 61.9%; Score 39; DB 6; Length 688;
 Best Local Similarity 77.8%; Pred. No. 3.5e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENG1L 9
 Db 672 IPVLDENG1M 680

Query Match 61.9%; Score 39; DB 6; Length 688;
 Best Local Similarity 77.8%; Pred. No. 1.e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENG1FAP 12
 Db 2077 IPNLGKGGLFAP 2088

Sequence 2893 AA;

Query Match 61.9%; Score 39; DB 6; Length 2893;
 Best Local Similarity 66.7%; Pred. No. 1.e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENG1FAP 12
 Db 2077 IPNLGKGGLFAP 2088

Sequence 2893 AA;

Query Match 61.9%; Score 39; DB 6; Length 2893;
 Best Local Similarity 66.7%; Pred. No. 1.e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENG1FAP 12
 Db 2077 IPNLGKGGLFAP 2088

Sequence 2893 AA;

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis

XX

CC polynucleotide molecules, polypeptides or monospecific antibodies;
 CC methods for detecting the presence of Helicobacter in samples using e.g.
 CC the polypeptides or monospecific antibodies; and methods for purifying
 CC the polypeptides by antibody-based affinity chromatography.

SQ Sequence 2893 AA;

Query Match Score 39; DB 2; Length 2893;
 Best Local Similarity Pred. No. 1.9e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 IPVLDENGIFAP 12
 Db 2077 IPNLGKKGIFAP 2088

RESULT 27

ABU30749 ABU30749 standard; protein; 2893 AA.

XX DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #16276.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Helicobacter pylori.

XX PN WO20027183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-0094893.

PR 25-OCT-2001; 2001US-034293P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Hasselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA34619.

New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 58673; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/patent/published_pct_sequences

XX SQ Sequence 2893 AA;

Query Match Score 39; DB 6; Length 2893;
 Best Local Similarity 61.9%; Pred. No. 1.3e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFAP 12
 Db 2077 IPNLGKKGIFAP 2088

RESULT 28

AAB48120 AAB48120 standard; peptide; 51 AA.

XX AC AAB48120;

XX DT 02-APR-2001 (first entry)

XX DE Consensus thyroglobulin type 1 domain.

XX XX TANGO 204; TANGO 206; TANGO 209; A236; secreted protein; human; mouse;
 KW transmembrane protein; antianemic; cerebroprotective; arteriosclerosis;
 KW antiasthmatic; neuroprotective; cytostatic; cardiotonic; hepatotoxic;
 KW antiinflammatory; antidiabetic; antiinflammatory; antipyretic; vasotropics;
 KW anti rheumatic; nephrotropic; hemostatic; antihypemic; osteopathic;
 KW ophthalmological; antisickling; anticancer; pulmonary; thyroglobulin.
 XX Unidentified.

XX DE AAB48120

XX XX TANGO 204; TANGO 206; TANGO 209; A236; secreted protein; human; mouse;
 KW transmembrane protein; antianemic; cerebroprotective; arteriosclerosis;
 KW antiasthmatic; neuroprotective; cytostatic; cardiotonic; hepatotoxic;
 KW antiinflammatory; antidiabetic; antiinflammatory; antipyretic; vasotropics;
 KW anti rheumatic; nephrotropic; hemostatic; antihypemic; osteopathic;
 KW ophthalmological; antisickling; anticancer; pulmonary; thyroglobulin.

XX OS Unidentified.

XX XX WO20069885-A2.

XX XX PD 23-NOV-2000.

XX XX PF 15-MAY-2000; 2000WO-US013361.

XX XX PR 14-MAY-1999; 990US-00312359.

XX XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Pan Y, Leiby KR;

XX XX Disclosure; Fig 16; 20pp; English.

DR WPI; 2001-024999/03.

XX The invention provides human and mouse nucleic acids designated TANGO
 CC 204, TANGO 206, TANGO 209 and A236 encoding secreted or transmembrane
 CC proteins. The polypeptides, nucleic acids and their modulators may be
 CC useful for treating, e.g. cancer, hemophilia, anemia, ischemia or diseases of
 CC the lung, liver, kidney or pancreas.

XX XX Disclosure; Fig 16; 20pp; English.

PT Novel nucleic acids encoding secreted or transmembrane proteins, useful
 PT for treating, e.g. cancer, hemophilia, anemia, ischemia or diseases of
 PT the lung, liver, kidney or pancreas.

XX XX Disclosure; Fig 16; 20pp; English.

CC The invention provides human and mouse nucleic acids designated TANGO
 CC 204, TANGO 206, TANGO 209 and A236 encoding secreted or transmembrane
 CC proteins. The polypeptides, nucleic acids and their modulators may be
 CC useful for treating or modulating cholesterol uptake, blood coagulation,
 CC to modulate cell proliferation, morphogenesis and fate specification,
 CC tissue repair and renewal, to treat cancer and promote wound healing,
 CC modulate angiogenesis, treat hypercholesterolemia, hemophilia, Marfan
 CC syndrome, protein S deficiency, modulate allergic or inflammatory

CC invention.
 XX Sequence 197 AA;
 SQ Query Match 60.3%; Score 38; DB 7; Length 197;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;
 Qy 2 PYLDENGL 9
 1 | | | |
 Db 3 PYFDENG 10
 1 | | | |

RESULT 31
 ABP66209 standard; protein; 213 AA.
 ID ABP66209 standard; protein; 213 AA.
 XX AC AAGG2332;
 XX DT 19-NOV-2002 (first entry)
 XX DB Bifidobacterium longum NCCT2705 ORF amino acid sequence SEQ ID NO:953.
 KW Bifidobacterium longum NCCT2705; Bifidobacterium; bacterial;
 KW identiaffrication; antibacterial; inhibitor of Salmonella; detection;
 KW rotavirus; food composition; pharmaceutical composition.
 KW OS Bifidobacterium longum.
 XX PN EP1227152-A1.
 XX PD 31-JUL-2002.
 XX PF 30-JAN-2001; 2001EP-00102050.
 XX PR 30-JAN-2001; 2001EP-00102050.
 XX PA (NEST) SOC PROD NESTLE SA.
 XX WPI: 2002-668397/72.
 XX PT Novel polynucleotide comprising Bifidobacterium genome sequence useful as
 PT a probe or primer for detecting and/or identifying Bifidobacterium longum
 PT in a biological sample.
 XX PS Claim 3; SEQ ID NO 953; 80pp; English.
 XX CC The present invention describes a polynucleotide (I) comprising a
 CC sequence of a Bifidobacterium Genome selected from the nucleotide
 CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at
 CC least 90% identity or which hybridises with the sequences given in
 CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a
 CC fusion protein, comprising a sequence selected from 1097 sequences given
 CC in ABP6258 to ABP6354 ligated in frame to poly nucleotide encoding a
 CC heterologous polypeptide. (I) has anti diarrhoeal and antibacterial
 CC activities, and can be used as an inhibitor of Salmonella. (I) (which is
 CC a probe) is useful for the detection and/or identification of
 CC Bifidobacterium longum in a biological sample. A carrier containing the
 CC lactic acid bacterium Bifidobacterium longum NCCT2705 (CNCM I-2618) can be
 CC used for preventing and/or treating diarrhoea brought about by pathogenic
 CC bacteria and/or rotavirus. The carrier is a food composition selected
 CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented
 CC products, ice-creams, fermented cereal based products, milk based
 CC powders, infant formula, pet food or a pharmaceutical composition
 CC selected from tablets, liquid bacterial suspensions, dried oral
 CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
 CC (I) is useful in DNA arrays or chips to carry out analysis of the
 CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
 CC Bifidobacterium related nucleotide sequences given in the Sequence
 CC Listing from the present invention but not mentioned further within the
 CC specification. N.B. The sequence data for this patent is not represented
 CC in the printed specification but is based on sequence information

CC supplied by the European Patent Office
 XX Sequence 213 AA;
 SQ Query Match 60.3%; Score 38; DB 5; Length 213;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;
 Qy 3 VLDENGLFAP 12
 1 | | | | | |
 Db 17 WWDENGFFVFP 26
 XX

RESULT 32
 AAGG2332 standard; protein; 313 AA.
 ID AAGG2332;
 XX AC AAGG2332;
 XX DT 03-SEP-2001 (first entry)
 XX DB S. epidermidis open reading frame protein sequence SEQ ID NO:1758.
 KW Staphylococcus epidermidis SRL strain; infection; diagnosis; vaccination;
 KW endocarditis.
 XX OS Staphylococcus epidermidis.
 XX PN WO200134809-A2.
 XX PD 17-MAY-2001.
 XX PP 09-NOV-2000; 2000WO-US030782.
 XX PR 09-NOV-1999; 99US-0164258P.
 XX PA (GLAXO) GLAXO GROUP LTD.
 XX PI Kimmerly WJ;
 XX DR WPI: 2001-316495/33.
 XX N-PSDB; AAH51182.
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 PT useful for vaccinating against infections, e.g. endocarditis.
 XX PS Claim 18; Page 486; 2188pp; English.

CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
 CC (II), given in AAC81454 to AAC81450, from Staphylococcus epidermidis. (I)
 CC and (II) can have antibacterial activity and therefore can be used in
 CC epidermidis. The nucleic acids (I) may be used to produce the S.
 CC epidermidis polypeptides (II) via the production of vectors containing
 CC them which are used to produce host cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
 CC used to vaccinate subjects and to raise antibodies against the bacteria.
 CC The polypeptides may also be used to assay for other inhibitors of their
 CC activity and therefore identify compounds that may be used for the
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
 CC AAH53970 represent specifically claimed S. epidermidis genomic DNA,
 CC polynucleotide sequences from the present invention. AAH5091 to AAH55098
 CC represent oligonucleotide sequences and primers which are used in the
 CC exemplification of the present invention N.B. The present invention
 CC specifically claims all the polynucleotide sequences given in the
 CC sequence listing of the present specification, however the sequence
 CC listing only goes up to SEQ ID NO:4444 so even though sequences are given
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
 CC for SEQ ID NO:4455 to 4464
 XX SQ Sequence 313 AA;
 Query Match 60.3%; Score 38; DB 4; Length 313;
 Best Local Similarity 77.8%; Pred. No. 2.1e+02;

Matches	7;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;		
Qy	2	PVLDENG1P 10								XX	06-MAY-2004 (first entry)
Db	64	PTLDGLGP 72								DT	
RESULT 33											
ID	ABR52942	standard; protein; 322 AA.								XX	Disease treating protein complex-derived protein #134.
XX		ABR52942								XX	KW
AC										XX	protein complex; drug target; diagnosis.
XX										OS	Unidentified.
DT										XX	
XX										PN	EP138608-A2.
XX										XX	
XX										PD	27-AUG-2003.
XX										XX	
DE										PF	20-DBC-2002; 2002EP-00102902.
XX										XX	
DE		Protein sequence #SEQ ID 749.								PR	20-DBC-2001; 2001EP-00130253.
XX										XX	
KW		Multiprotein complex; eukaryote; drug target; diagnosis.								PA	(CELL-) CELLZONE AG.
OS		Saccharomyces cerevisiae.								PI	Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J, Kruse U, Merino A, Bauch A;
XX										PI	Marzioch M, Grandi P,
OS		EP1258494-A1.								PI	Michon A, Leutwein C, Rick J;
XX										XX	WPI:2003-6386460/61.
PD		20-NOV-2002.								DR	N-PDB; ADK62017.
XX										XX	
PF		20-DEC-2001; 2001EP-00130253.								PR	New proteins and protein complexes from eukaryotes, useful as targets in
XX										PR	drug screening, or in diagnosing or screening for the presence of a
PR		15-MAY-2001; 2001EP-00111774.								PR	disease or disorder, or a predisposition for developing a disease or
XX										PR	disorder in a subject.
PA		(CELL-) CELLZONE AG.								XX	
PI		Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;								PS	Disclosure: SEQ ID NO 267; 13pp; English.
PI		PI Marzioch M, Schultz JD, Superti-Furga GD;								XX	
XX										CC	The invention relates to novel protein complexes comprising a first and a
WPI		2003-250078/25.								CC	second protein, or its derivative, fragment, homologue or variant. The
DR		DR N-PSDB; ACC60984.								CC	proteins are selected from given protein complexes, which are not defined
XX										CC	in the specification. The variants are encoded by nucleic acids that
XX		New isolated protein complexes useful for diagnosing a disease or								CC	hybridize to the nucleic acids encoding the proteins under low stringency
PT		PT disorder, or as a target for an active agent of a pharmaceutical,								CC	conditions. The protein complexes are useful as targets for an active
PT		preferably a drug target in the treatment or prevention of disease or								CC	agent of a pharmaceutical. These protein complexes are particularly
PT		disorder.								CC	useful as drug targets for the treatment or preventing of a disease or
XX										CC	disorder. The complexes and methods above are useful in diagnosing or
XX		Disclosure: SEQ ID NO 749; 17pp + Sequence Listing; English.								CC	screening for the presence of a disease or disorder in a subject. These are also useful
XX										CC	CC in screening for a drug for treatment or prevention of a disease or
XX		CC disorder. The molecule that modulates the amount, activity or protein								CC	CC components of the complex is useful for the manufacture of a medicament
XX		CC obtainable by using a protein as a bait and isolating the set of proteins								CC	CC for the treatment or prevention of a disease or disorder. This sequence
CC		CC which is attached thereto from cells. Such protein complexes may comprise								CC	CC corresponds to a protein of the invention. (Note: the sequence data for
CC		CC up to 30 distinct proteins. Protein complexes of the invention are useful								CC	CC this patent did not form part of the printed specification but was
CC		CC for diagnosing a disease or disorder, or as a target for an active agent								CC	CC obtained from the EPO in electronic format).
CC		CC of a pharmaceutical, preferably a drug target in the treatment or								XX	XX
CC		CC prevention of a disease or disorder. Note: The sequence data for this								SQ	Sequence 322 AA;
CC		CC patent is not represented in the printed specification, but is based on								Query Match	60.3%; Score 38; DB 7; Length 322;
CC		CC sequence information supplied by the European Patent Office. The complete								Best Local Similarity	62.5%; Pred. No. 2.2e+02;
CC		CC document is available on CD-ROM								Matches	3; Mismatches 0; Indels 0; Gaps 0;
XX		Sequence 322 AA;								Qy	1 IPVLDENG 8
XX										ID	ABP18384 standard; protein; 328 AA.
XX		Query Match 60.3%; Score 38; DB 6; Length 322;								XX	
XX		Best Local Similarity 62.5%; Pred. No. 2.2e+02;								Db	223 VPIIDENG 230
XX		Matches 3; Mismatches 0; Indels 0; Gaps 0;								RESULT 35	
XX										ABP18384	
XX		Qy 1 IPVLDENG 8								AC	
XX		Db 223 VPIIDENG 230								XX	
XX										AC	
XX		Query Match 60.3%; Score 38; DB 7; Length 322;								XX	
XX		Best Local Similarity 62.5%; Pred. No. 2.2e+02;								Db	24-JUL-2002 (first entry)
XX		Matches 3; Mismatches 0; Indels 0; Gaps 0;								RESULT 34	
XX										ID	ADK62016
XX		Qy 1 IPVLDENG 8								XX	ID ADK62016 standard; protein; 322 AA.
XX		Db 223 VPIIDENG 230								XX	XX
XX										AC	Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3229.
XX		XX								AC	ADK62016;

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy.
 XX
 OS Staphylococcus epidermidis.
 XX US6380370-B1.
 PN
 XX 30-APR-2002.
 PD
 XX PP 13-AUG-1998; 98US-00134001.
 PR 14-AUG-1997; 97US-0055779P.
 DR 08-NOV-1997; 97US-0064964P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Doucette-Stamm LA, Bush D;
 DR; WPI; 2002-281255/41.
 DR N-PSDB; ABR90929.
 XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections.
 XX Disclosure; SEQ ID NO 3229; 267pp; English.
 CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP7960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
 XX SQ Sequence 328 AA;
 Query Match 60.3%; Score 38; DB 5; Length 328;
 Best Local Similarity 77.8%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PVLDEGLF 10
 :||| |||
 Db 79 PILDEGLF 87
 Sequence 483 AA;
 RESULT 36
 ABU20549
 ID ABU20549 standard; protein; 483 AA.
 XX AC ABU20549;
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #6076.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Bacteroides fragilis.
 XX WO200277183-A2.
 PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0343923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskard JW;
 PI Wall D, Trawick JD, Carr GA, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA24419.
 XX PS Claim 25; SEQ ID NO 48473; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; or (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (8) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 483 AA;
 Query Match 60.3%; Score 38; DB 6; Length 483;
 Best Local Similarity 58.3%; Pred. No. 3.5e+02;
 Matches 3; Mismatches 2; Indels 0; Gaps 0;
 XX AC AAG31867;
 AC AAG31867;
 DT 17-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 38342.
 XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.

XX	PN	EP1033405-A2.	990US-0141842P.
XX	PD	06-SEP-2000.	990US-0142154P.
XX	PP	25-FEB-2000; 2000EP-00301439.	990US-012055P.
PR	05-MAR-1999;	990US-0121825P.	990US-012390P.
PR	09-US-0123548P.	990US-0142803P.	
PR	23-MAR-1999;	990US-0123788P.	990US-0142920P.
PR	25-MAR-1999;	990US-0124264P.	990US-0142977P.
PR	29-US-01246785P.	990US-0143542P.	
PR	01-APR-1999;	990US-01247462P.	990US-0143624P.
PR	06-APR-1999;	990US-01282334P.	990US-014331P.
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 XX ID AAG31866 standard; protein; 582 AA. PR 23-JUN-1999; 99US-0140353P.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence. PR 23-JUN-1999; 99US-0140354P.
 OS Arabidopsis thaliana. PR 24-JUN-1999; 99US-0140695P.
 XX AC AAG31866; PR 28-JUN-1999; 99US-0140823P.
 XX DT 17-OCT-2000 (first entry) PR 29-JUN-1999; 99US-0140991P.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 38341. PR 30-JUN-1999; 99US-0141287P.
 XX ID AAG31866 standard; protein; 582 AA. PR 01-JUL-1999; 99US-0141842P.
 XX AC AAG31866; PR 01-JUL-1999; 99US-0142154P.
 XX DT 06-SEP-2000. PR 02-JUL-1999; 99US-0142055P.
 XX PD 06-SEP-2000. PR 06-JUL-1999; 99US-0142390P.
 XX PF 25-FEB-2000; 2000EP-00301439. PR 09-JUL-1999; 99US-0142920P.
 XX PR 12-JUL-1999; 99US-0142977P.

Query Match 60.3%; Score 38; DB 3; Length 515;
 Best Local Similarity 100.0%; Pred. No. 3.8e-02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLDENG 8
 Db 195 PVLDENG 201

RESULT 38

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XX AC AAG31866;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 38341.

XX ID AAG31866 standard; protein; 582 AA.

XX AC AAG31866;

XX DT 06-SEP-2000.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

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PR	04-AUG-1999;	99US-0147308P.	PR	28-OCT-1999;	99US-0161993P.
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PR	20-AUG-1999;	99US-0149722P.	XX		
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PR	15-SEP-1999;	99US-0154018P.	XX		
PR	16-SEP-1999;	99US-0154039P.	PR	28-SEP-2001; 2001US-0368133P.	
PR	31-AUG-1999;	99US-0154438P.	PR	15-APR-2002; 2002US-0373225P.	
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PR	29-SEP-1999;	99US-0156596P.	XX		

PI	Simmons D,	Chandrasekharan VN;
XX	DR	2003-421222/39.
XX	WPI;	2003-421222/39.
XX	Novel cyclooxygenase type 1 variant polypeptide and a polynucleotide encoding the polypeptide, useful for identifying a compound that binds to and modulates the activity of COX-1 variant polypeptide.	
PT	PT	Claim 18; SEQ ID NO 14; 150pp; English.
PR	CC	The present invention describes an isolated cyclooxygenase type 1 (COX-1) variant polypeptide (1). (1) is useful for identifying a compound which modulates the activity of (1). A nucleotide sequence encoding (1) can be used for mapping their respective genes on a chromosome and so locating gene regions associated with genetic disease, identifying an individual from a minute biological sample (tissue typing), and to aid in forensic identification of a biological sample. The present sequence represents a sequence which is used in the exemplification of the present invention.
PS	CC	Sequence 613 AA:
XX	CC	Sequence 613 AA:
Qy	Query Match Score 38; DB 7; Length 613; Best Local Similarity 58.3%; Pred. No. 4.7e-02; Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	
Db	1 IPVLDENGFLPAP 12 84 LPVLPHGHLFRP 95	
AC	AAG31865	
XX	RESULT 40	
DT	17-OCT-2010 (First entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 38340.	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 38340.	
XX	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; generic mapping; gene expression control; promoter; termination sequence.	
KW	KW	
OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PN	06-SEP-2000.	
PD	06-SEP-2000.	
XX	PPF 25-FEB-2000; 20000EP-00301439.	
XX	PR 25-FEB-1999; 99US-0121825P.	
PR	05-MAR-1999; 99US-0123180P.	
PR	09-MAR-1999; 99US-0123548P.	
PR	23-MAR-1999; 99US-0125788P.	
PR	25-MAR-1999; 99US-0126264P.	
PR	29-MAR-1999; 99US-0126785P.	
PR	01-APR-1999; 99US-0127462P.	
PR	06-APR-1999; 99US-0130510P.	
PR	23-APR-1999; 99US-0130891P.	
PR	08-APR-1999; 99US-0128714P.	
PR	16-APR-1999; 99US-0129845P.	
PR	19-APR-1999; 99US-0130077P.	
PR	21-APR-1999; 99US-0130449P.	
PR	23-APR-1999; 99US-0132485P.	
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PR	20-JUL-1999; 99US-0144333P.	
PR	21-JUL-1999; 99US-0144334P.	
PR	21-JUL-1999; 99US-0145086P.	
PR	22-JUL-1999; 99US-0145085P.	
PR	22-JUL-1999; 99US-0145087P.	
PR	22-JUL-1999; 99US-01451929P.	
PR	22-JUL-1999; 99US-01452089P.	
PR	22-JUL-1999; 99US-01452101P.	

		Query Match	Score	DB 3;	DB 3;
		Best Local Similarity	100.0%;	Pred. No.	Mismatches
		Matches	0;	7	0;
Qy	Db	PVLDENG 8 300 PVLDENG 306			
PR 23-JUL-1999;	99US-0145145P.				
PR 23-JUL-1999;	99US-0145218P.				
PR 23-JUL-1999;	99US-0145224P.				
PR 26-JUL-1999;	99US-0145377P.				
PR 27-JUL-1999;	99US-0145913P.				
PR 27-JUL-1999;	99US-0145918P.				
PR 27-JUL-1999;	99US-0145919P.				
PR 28-AUG-1999;	99US-0145951P.				
PR 02-AUG-1999;	99US-0145986P.				
PR 02-AUG-1999;	99US-0146388P.				
PR 02-AUG-1999;	99US-0146389P.				
PR 03-AUG-1999;	99US-0147038P.				
PR 04-AUG-1999;	99US-0147204P.				
PR 04-AUG-1999;	99US-0147302P.				
PR 05-AUG-1999;	99US-0147319P.				
PR 06-AUG-1999;	99US-0147426P.				
PR 06-AUG-1999;	99US-0147430P.				
PR 09-AUG-1999;	99US-0147416P.				
PR 09-AUG-1999;	99US-0147435P.				
PR 10-AUG-1999;	99US-0148171P.				
PR 11-AUG-1999;	99US-0148319P.				
PR 12-AUG-1999;	99US-0148341P.				
PR 13-AUG-1999;	99US-0148565P.				
PR 13-AUG-1999;	99US-0148684P.				
PR 16-AUG-1999;	99US-0149368P.				
PR 17-AUG-1999;	99US-0149175P.				
PR 18-AUG-1999;	99US-0149261P.				
PR 20-AUG-1999;	99US-0149322P.				
PR 20-AUG-1999;	99US-0149723P.				
PR 23-AUG-1999;	99US-0149929P.				
PR 23-AUG-1999;	99US-0149902P.				
PR 23-AUG-1999;	99US-0149930P.				
PR 25-AUG-1999;	99US-0150566P.				
PR 26-AUG-1999;	99US-0150884P.				
PR 27-AUG-1999;	99US-0151065P.				
PR 27-AUG-1999;	99US-0151066P.				
PR 27-AUG-1999;	99US-0151080P.				
PR 31-AUG-1999;	99US-0151303P.				
PR 01-SEP-1999;	99US-0151438P.				
PR 07-SEP-1999;	99US-0151930P.				
PR 10-SEP-1999;	99US-0152363P.				
PR 13-SEP-1999;	99US-0153070P.				
PR 15-SEP-1999;	99US-0153758P.				
PR 16-SEP-1999;	99US-0154018P.				
PR 29-SEP-1999;	99US-0154039P.				
PR 04-OCT-1999;	99US-0154779P.				
PR 05-OCT-1999;	99US-0155139P.				
PR 06-OCT-1999;	99US-0155294P.				
PR 07-OCT-1999;	99US-0155855P.				
PR 14-OCT-1999;	99US-0156029P.				
PR 14-OCT-1999;	99US-0156232P.				
PR 14-OCT-1999;	99US-0156330P.				
PR 14-OCT-1999;	99US-0156331P.				
PR 14-OCT-1999;	99US-0156373P.				
PR 14-OCT-1999;	99US-0156388P.				
PR 18-OCT-1999;	99US-015554P.				
PR 21-OCT-1999;	99US-016041P.				
PR 21-OCT-1999;	99US-0160767P.				
PR 21-OCT-1999;	99US-0160768P.				
PR 21-OCT-1999;	99US-0160814P.				
PR 21-OCT-1999;	99US-0160815P.				

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OM protein - protein search, using sw mode1

Run on: January 7, 2005, 10:02:01 ; Search time 26 Seconds
(without alignments)
30.608 Million cell updates/sec

Title: US-09-699-224A-1
Perfect score: 63
Sequence: 1 IPVLDENGIFAP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
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6: /cgn2_6/podata/1/iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	41	65.1	64	4	US-09-328-352-6518	Sequence 6518, Ap	
2	40	63.5	441	4	US-09-328-352-7754	Sequence 7754, Ap	
3	38	60.3	313	4	US-09-328-352-1758	Sequence 1758, Ap	
4	38	60.3	322	3	US-09-359-161-7	Sequence 7, Appli	
5	38	60.3	322	4	US-09-538-092-287	Sequence 297, App	
6	38	60.3	328	3	US-09-134-001C-3229	Sequence 322, Ap	
7	38	60.3	588	4	US-09-248-796A-20295	Sequence 20295, A	
8	38	60.3	712	4	US-09-708-426-9	Sequence 9, Appli	
9	37.5	59.5	1646	4	US-09-583-110-4667	Sequence 4667, Ap	
10	37	58.7	104	3	US-09-946-329A-97	Sequence 97, Appli	
11	37	58.7	174	4	US-09-903-456-40	Sequence 40, Appli	
12	37	58.7	178	4	US-09-145-828A-24	Sequence 24, Appli	
13	37	58.7	178	4	US-09-903-456-26	Sequence 26, Appli	
14	37	58.7	219	4	US-09-903-456-38	Sequence 38, Appli	
15	37	58.7	221	4	US-09-543-681A-1514	Sequence 4514, Ap	
16	37	58.7	241	4	US-09-248-796A-15234	Sequence 15234, A	
17	37	58.7	280	4	US-09-145-828A-21	Sequence 21, Appli	
18	37	58.7	280	4	US-09-903-456-28	Sequence 28, Appli	
19	37	58.7	286	4	US-09-903-456-59	Sequence 59, Appli	
20	37	58.7	289	4	US-09-145-828A-17	Sequence 17, Appli	
21	37	58.7	289	4	US-09-903-456-21	Sequence 21, Appli	
22	37	58.7	289	4	US-09-903-456-34	Sequence 34, Appli	
23	37	58.7	291	4	US-09-903-456-36	Sequence 36, Appli	
24	37	58.7	293	4	US-09-145-828A-12	Sequence 12, Appli	
25	37	58.7	293	4	US-09-903-456-19	Sequence 19, Appli	
26	37	58.7	301	4	US-09-903-456-33	Sequence 33, Appli	
27	37	58.7	317	4	US-09-145-828A-7	Sequence 7, Appli	

ALIGNMENTS

RESULT 1
US-09-328-352-6518
; Sequence 6518, Application US/09328352
; Patent No. 656298
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6518
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-6518

Query Match 65.1%; Score 41; DB 4; Length 64;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VLDENGIFAP 12
Db 36 VLDENGILKP 45

RESULT 2
US-09-328-352-7754
; Sequence 7754, Application US/09328352
; Patent No. 656298
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7754
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-7754

Query Match 63.5%; Score 40; DB 4; Length 441;
Best Local Similarity 58.3%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFAP 12
Db 1 IPVLDENGLKP 45

Qy

Db 118 LPTYDQVGLFAP 129

RESULT 5
US-09-538-092-297
; Sequence 297, Application US/09538092

; Patent No. 6733314
; GENERAL INFORMATION:
; APPLICANT: KIMMERY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1758
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1758

Query Match Score 38; DB 4; Length 313;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PVLDENGFLF 10
Db 64 PILDEGLF 72

RESULT 4
US-09-359-161-7
; Sequence 7, Application US/09359161A

; Patent No. 6342656
; GENERAL INFORMATION:
; APPLICANT: Bradford, Kent J.
; APPLICANT: Dhal, Peetambar
; APPLICANT: Yang, Hong
; APPLICANT: Cooley, Michael
; APPLICANT: Downie, Bruce
; APPLICANT: Gee, Oliver
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Regulation of Source Sink Relationships and Responses
; TITLE OF INVENTION: to Stress Conditions in Plants
; FILE REFERENCE: 023070-09390US
; CURRENT APPLICATION NUMBER: US/09/359,161A
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

Query Match Score 38; DB 3; Length 322;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENG 8
Db 223 VPIIDENG 230

RESULT 5
US-09-538-092-297
; Sequence 297, Application US/09538092

; Patent No. 6733314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,955
; PRIOR FILING DATE: 2000-04-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapetSeqFormatter Version 0.9
; SEQ ID NO: 297
; LENGTH: 322
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YGL115W
US-09-538-092-297

Query Match Score 38; DB 4; Length 322;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENG 8
Db 223 VPIIDENG 230

RESULT 6
US-09-134-001C-3229
; Sequence 3229, Application US/09134001C

; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lydie Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 3229
; LENGTH: 328
; TYPE: PRT
; ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-3229

Query Match Score 38; DB 3; Length 328;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PVLDENG 10
Db 79 PILDEGLF 87

RESULT 7
US-09-248-796A-20295
; Sequence 20295, Application US/0924896A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

Query Match Score 38; DB 3; Length 328;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENG 8
Db 223 VPIIDENG 230

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 50/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 20295
 LENGTH: 588
 TYPE: PRT
 ORGANISM: *Candida albicans*
 US-09-248-796A-20295

Query Match 60.3%; Score 38; DB 4; Length 588;
 Best Local Similarity 70.0%; Pred. No. 90;
 Matches 7; Conservative 2; Mismatches 1; Indels 0;
 Gaps 0;

Qy 1 IPVLDENGIF 10
 Db 525 IPVVDDEDSLIP 534

RESULT 8
 US-09-708-426-9
 Sequence 9, Application US/09708426
 Patent No. 6444429
 GENERAL INFORMATION:
 APPLICANT: HAN, YE-SUN
 APPLICANT: YU, YEON-GYU
 APPLICANT: LIM, JAE-HWAN
 TITLE OF INVENTION: GENE CODING FOR DNA LIGASE OF HYPERTHERMOPHILIC BACTERIA AQUIFER
 FILE REFERENCE: 1995579US0
 CURRENT APPLICATION NUMBER: US/09/708,426
 CURRENT FILING DATE: 2000-11-09
 PRIOR FILING DATE: 1999-11-10
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 9
 LENGTH: 712
 TYPE: PRT
 ORGANISM: *Rhodothermus marinus*
 US-09-708-426-9

Query Match 60.3%; Score 38; DB 4; Length 712;
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 IPVLDENGIF 9
 Db 697 IPMLDDEGIL 705

RESULT 9
 US-09-583-110-4667
 Sequence 4667, Application US/09583110
 Patent No. 6699703
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to *Streptococcus pneumoniae*
 FILE REFERENCE: PATH00-07A
 CURRENT APPLICATION NUMBER: US/09/583,110
 CURRENT FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/107,433
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/085,131
 PRIOR FILING DATE: 1998-05-12
 PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02
 NUMBER OF SEQ ID NOS: 5322
 SEQ ID NO: 4667
 LENGTH: 1646
 TYPE: PRT
 ORGANISM: *Streptococcus pneumoniae*
 US-09-583-110-4667

Query Match 59.5%; Score 37.5; DB 4; Length 1646;
 Best Local Similarity 59.9%; Pred. No. 3.7e+02;
 Matches 9; Conservative 1; Mismatches 0; Indels 7;
 Gaps 1;

Qy 3 VLDEN-----GLFAP 12
 Db 444 ILDENGKLRLSGLFAP 460

RESULT 10
 US-08-946-329A-97
 Sequence 97, Application US/08946329A
 Patent No. 6057091
 GENERAL INFORMATION:
 APPLICANT: Beachy, Philip A.
 APPLICANT: Porter, Jeffrey A.
 TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 NUMBER OF SEQUENCES: 109
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/946,329A
 FILING DATE: 07-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/061,323
 FILING DATE: 07-OCT-1996
 APPLICATION NUMBER: 08/729,743
 FILING DATE: 10-JUL-1996
 APPLICATION NUMBER: 08/567,357
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/349,498
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/140001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5059
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-946-329A-97

Query Match 58.7%; Score 37; DB 3; Length 104;
 Best Local Similarity 72.7%; Pred. No. 18;
 Matches 8; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

Qy 1 IPVLDENGIF 11
 Db 40 IMMLDENGLVA 50

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RESULT 11
US-09-903-456-40
Sequence 40, Application US/0903456
GENERAL INFORMATION: Patent No. 6677145
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Pereira, Suzette L.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903_456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624, 670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379, 095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145, 828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 40
LENGTH: 174
TYPE: PRT
ORGANISM: Mortierella alpina
RESULT 12
US-09-903-456-40
Query Match
Best Local Similarity 60.0%; Score 37; DB 4; Length 174;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENGIF 10
Db 80 VPILARNLIF 89
RESULT 13
US-09-903-456-24
Sequence 24, Application US/09145828A
GENERAL INFORMATION: Patent No. 6603349
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.OI
CURRENT APPLICATION NUMBER: US/09/145, 828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 24
LENGTH: 178
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
RESULT 14
US-09-903-456-38
Sequence 38, Application US/09903456
GENERAL INFORMATION: Patent No. 6677145
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903_456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624, 670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379, 095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145, 828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 38
LENGTH: 219
TYPE: PRT
ORGANISM: Mortierella alpina
RESULT 15
US-09-903-456-26
Query Match
Best Local Similarity 60.0%; Score 37; DB 4; Length 219;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENGIF 10
Db 10 VPILARNLIF 19

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US-09-543-681A-4514 ; CURRENT APPLICATION NUMBER: US/09/145,828A
; Sequence 4514, Application US/09543681A
; Patent No. 6605709 ; CURRENT FILING DATE: 1998-09-02
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON ; NUMBER OF SEQ ID NOS: 30
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS ; SOFTWARE: FastSEQ for Windows Version 4.0
; FILE REFERENCE: 2709 1002-001 ; SEQ ID NO: 21
; LENGTH: 280 ;
; CURRENT APPLICATION NUMBER: US/09/543,681A ;
; CURRENT FILING DATE: 2000-04-05 ;
; PRIORITY NUMBER: US 60/128,706 ;
; PRIOR APPLICATION NUMBER: US 60/128,706 ;
; PRIOR FILING DATE: 1999-04-09 ;
; NUMBER OF SEQ ID NOS: 8344 ;
; SEQ ID NO: 4514 ;
; LENGTH: 221 ;
; TYPE: PRT ;
; ORGANISM: Proteus mirabilis ;
; US-09-543-681A-4514

Query Match 58.7%; Score 37; DB 4; Length 221;
Best Local Similarity 72.7%; Pred. No. 43; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGFLPA 11
Db 63 IPVLDQATLFLPA 73

RESULT 16

US-09-248-796A-15234 ; CURRENT APPLICATION NUMBER: US/09248796A
; Sequence 15234, Application US/09248796A
; Patent No. 6747137 ; CURRENT FILING DATE: 2001-07-11
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al ; NUMBER OF SEQ ID NOS: 116
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN ; SOFTWARE: FastSEQ for Windows Version 4.0
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS ;
; FILE REFERENCE: 107196.132 ;
; CURRENT APPLICATION NUMBER: US/09/248,796A ;
; CURRENT FILING DATE: 1999-02-12 ;
; PRIORITY NUMBER: US 60/074,725 ;
; PRIOR FILING DATE: 1998-02-13 ;
; PRIORITY NUMBER: US 60/096,409 ;
; PRIOR FILING DATE: 1998-08-13 ;
; NUMBER OF SEQ ID NOS: 28208 ;
; SEQ ID NO: 15234 ;
; LENGTH: 241 ;
; TYPE: PRT ;
; ORGANISM: Candida albicans ;
; US-09-248-796A-15234

Query Match 58.7%; Score 37; DB 4; Length 241;
Best Local Similarity 60.0%; Pred. No. 48; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VLDDNGLFP 12
Db 214 LLDDQGLFP 223

RESULT 17

US-09-145-828A-21 ; CURRENT APPLICATION NUMBER: US/09145828A
; Sequence 21, Application US/09145828A
; Patent No. 6403319 ; CURRENT FILING DATE: 1998-09-02
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories ; NUMBER OF SEQ ID NOS: 20
; APPLICANT: Mukerji, Pradip ;
; APPLICANT: Leonard, Amanda E. Y. ;
; APPLICANT: Huang, Yung-Sheng ;
; APPLICANT: Thurmond, Jennifer ;
; APPLICANT: Kirchner, Stephen J. ;
; APPLICANT: Parker-Barnes, Jennifer M. ;
; TITLE OF INVENTION: THE BLONGASE GENE AND USES THEREOF ;
; FILE REFERENCE: 6407.US.01

Query Match 58.7%; Score 37; DB 4; Length 280;
Best Local Similarity 60.0%; Pred. No. 57; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGFL 10
Db 70 VPILARGLP 79

RESULT 19

US-09-903-456-59 ; CURRENT APPLICATION NUMBER: US/09903456
; Sequence 59, Application US/09903456
; Patent No. 6677145 ; CURRENT FILING DATE: 2001-07-11
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories ; NUMBER OF SEQ ID NOS: 116
; APPLICANT: Mukerji, Pradip ;
; APPLICANT: Leonard, Amanda Eun-Yeong ;
; APPLICANT: Huang, Yung-Sheng ;
; APPLICANT: Pereira, Suzette L. ;
; TITLE OF INVENTION: BLONGASE GENES AND USES THEREOF ;
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIORITY NUMBER: US 09/624,670 ;
; PRIOR FILING DATE: 2000-07-24
; PRIORITY NUMBER: US 09/379,095 ;
; PRIOR FILING DATE: 1999-08-23
; PRIORITY NUMBER: US 09/145,828 ;
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116 ;
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 28 ;
; LENGTH: 280 ;
; TYPE: PRT ;
; ORGANISM: Mortierella alpina ;
; FEATURE:
; NAME/KEY: VARIANT ;
; LOCATION: (280)...(280) ;
; OTHER INFORMATION: Xaa = Unknown or Other at position 280 ;
; US-09-903-456-59

Query Match 58.7%; Score 37; DB 4; Length 280;
Best Local Similarity 60.0%; Pred. No. 57; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGFL 10
Db 70 VPILARGLP 79

APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
 FILE REFERENCE: 6407.US.P3
 CURRENT APPLICATION NUMBER: US/09/903,456
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US/09/624,670
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: US/09/379,095
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: US/09/145,828
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 59
 LENGTH: 286
 TYPE: PRT
 ORGANISM: Mortierella alpina
 US-09-903-456-59

Query Match Score 58.7%; DB 4; Length 286;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGLF 10
 Db 77 VPILARNGLF 86

RESULT 20
 US-09-145-828A-17
 Sequence 17, Application US/09145828A
 ; GENERAL INFORMATION:
 ; Patent No. 6403349

APPLICANT: Abbott Laboratories
 ; APP: Mukerji, Pradip
 ; APP: Leonard, Amanda E. Y.
 ; APP: Huang, Yung-Sheng
 ; APP: Thurmond, Jennifer
 ; APP: Kirchner, Stephen J.
 ; APP: Parker-Barnes, Jennifer M.
 TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
 FILE REFERENCE: 6407.US.O1
 CURRENT APPLICATION NUMBER: US/09/145,828A
 CURRENT FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 17
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Mortierella alpina
 ; FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (289) ..(289)
 OTHER INFORMATION: Xaa = Unknown or other at position 289
 US-09-145-828A-17

Query Match Score 58.7%; DB 4; Length 289;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGLF 10
 Db 79 VPILARNGLF 88

RESULT 21
 US-09-903-456-21
 Sequence 21, Application US/09903456
 ; GENERAL INFORMATION:
 ; APP: Abbott Laboratories
 ; APP: Mukerji, Pradip
 ; APP: Leonard, Amanda E. Y.
 ; APP: Huang, Yung-Sheng

APPLICANT: Huang, Yung-Sheng
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
 FILE REFERENCE: 6407.US.P3
 CURRENT APPLICATION NUMBER: US/09/903,456
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US/09/624,670
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: US/09/379,095
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: US/09/145,828
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 21
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Mortierella alpina
 ; FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (289) ..(289)
 OTHER INFORMATION: Xaa = Unknown or Other at position 289
 US-09-903-456-21

Query Match Score 58.7%; DB 4; Length 289;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGLF 10
 Db 79 VPILARNGLF 88

RESULT 22
 US-09-903-456-34
 Sequence 34, Application US/09903456
 ; Patent No. 6677145
 ; GENERAL INFORMATION:
 ; APP: Abbott Laboratories
 ; APP: Mukerji, Pradip
 ; APP: Leonard, Amanda E. Y.
 ; APP: Huang, Yung-Sheng
 ; APP: Pereira, Suzette L.
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
 FILE REFERENCE: 6407.US.P3
 CURRENT APPLICATION NUMBER: US/09/903,456
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US/09/624,670
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: US/09/379,095
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: US/09/145,828
 PRIOR FILING DATE: 1998-09-02
 NUMBER OF SEQ ID NOS: 116
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 34
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Mortierella alpina
 US-09-903-456-34

Query Match Score 58.7%; DB 4; Length 289;
 Best Local Similarity 60.0%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGLF 10
 Db 80 VPILARNGLF 89

RESULT 23
 US-09-903-456-36
 Sequence 36, Application US/09903456

```

; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US/09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US/09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 36
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Mortierella alpina
US-09-903-456-36

Query Match 58.7%; Score 37; DB 4; Length 291;
Best Local Similarity 60.0%; Pred. No. 60; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Insertions 0; Deletions 0;

RESULT 24
US-09-145-828A-12
; Sequence 12, Application US/09145828A
; Patent No. 6403319
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407 US O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (293) . . .
; OTHER INFORMATION: Xaa = Unknown or other at position 293
US-09-145-828A-12

Query Match 58.7%; Score 37; DB 4; Length 293;
Best Local Similarity 60.0%; Pred. No. 60; Indels 2; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Insertions 0; Deletions 0;

RESULT 25
US-09-903-456-19
; Sequence 19, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US/09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US/09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 19
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (293) . . .
; OTHER INFORMATION: Xaa = Unknown or Other at position 293
US-09-903-456-19

Query Match 58.7%; Score 37; DB 4; Length 293;
Best Local Similarity 60.0%; Pred. No. 60; Indels 2; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Insertions 0; Deletions 0;

RESULT 26
US-09-903-456-33
; Sequence 33, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US/09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US/09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 33
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (301) . . .
; OTHER INFORMATION: Xaa = Unknown or Other at position 301
US-09-903-456-33

Query Match 58.7%; Score 37; DB 4; Length 301;
Best Local Similarity 60.0%; Pred. No. 62; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; Insertions 0; Deletions 0;

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Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0; Db 108 VPILARNGLF 117

RESULT 27
US-09-145-828A-7
Sequence 7, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer J.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.O1
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 7
LENGTH: 317
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-145-828A-7

Query Match 58.7%; Score 37; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 66; Mismatches 2; Indels 0; Gaps 0; Db 108 VPILARNGLF 117

Qy 1 IPVLDENGFL 10
Db 108 VPILARNGLF 117

RESULT 28
US-09-903-456-13
Sequence 13, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 317
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-903-456-13

Query Match 58.7%; Score 37; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 66; Mismatches 2; Indels 0; Gaps 0; Db 108 VPILARNGLF 117

Qy 1 IPVLDENGFL 10
Db 108 VPILARNGLF 117

RESULT 29
US-09-145-828A-19
Sequence 19, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.O1
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 318
TYPE: PRT
ORGANISM: Mortierella alpina
FEATURE:
NAME/KEY: VARIANT
LOCATION: (318)...(318)
OTHER INFORMATION: Xaa = Unknown or other at position 318
US-09-145-828A-19

Query Match 58.7%; Score 37; DB 4; Length 318;
Best Local Similarity 60.0%; Pred. No. 66; Mismatches 2; Indels 0; Gaps 0; Db 108 VPILARNGLF 117

Qy 1 IPVLDENGFL 10
Db 108 VPILARNGLF 117

RESULT 30
US-09-903-456-25
Sequence 25, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 318
TYPE: PRT
ORGANISM: Mortierella alpina
FEATURE:
NAME/KEY: VARIANT
LOCATION: (318)...(318)
OTHER INFORMATION: Xaa = Unknown or Other at position 318
US-09-903-456-25

Qy 1 IPVLDENGFL 10
Db 108 VPILARNGLF 117

Query Match Score 37; DB 4; Length 318;
 Best Local Similarity 60.0%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFP 10
 Db 108 VPILARINGLF 117

RESULT 31
 US-09-489-039A-10054
 Sequence 10054 Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 FILE REFERENCE: 2709 2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-11-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 10054
 LENGTH: 367
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-10054

Query Match Score 37; DB 4; Length 367;
 Best Local Similarity 60.0%; Pred. No. 79;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFP 10
 Db 297 VPLDNNNGKF 306

RESULT 32
 US-09-248-796A-10059
 Sequence 18059 Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 18059
 LENGTH: 409
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-18059

Query Match Score 37; DB 4; Length 409;
 Best Local Similarity 77.8%; Pred. No. 89;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LDENGIFAP 12
 Db 229 LDDEGLIAP 237

RESULT 34
 US-09-540-236-3512
 Sequence 3512 Application US/09540236
 Patent No. 6673910
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
 FILE REFERENCE: 709 2002-05-06
 CURRENT APPLICATION NUMBER: US/10/140,002
 CURRENT FILING DATE: 2002-05-06
 Prior Application removed - See Palm or File wrapper
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 404
 LENGTH: 436
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-140-002-404

Query Match Score 37; DB 4; Length 436;
 Best Local Similarity 50.0%; Pred. No. 96;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFAP 12
 Db 338 IPCLCDEDGYK 349

RESULT 35
 US-09-220-767-46419
 Sequence 46419 Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
FILE REFERENCE: File Reference: 7326_094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 46119
LENGTH: 301
TYPE: PRT
ORGANISM: *Drosophila melanogaster*

US-09-270-767-46419

Query Match Score 36; DB 4; Length 301;
Best Local Similarity 60.0%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VLDENGFLAP 12
Db 112 TASENGFLFPV 121

RESULT 36
US-08-311-731A-104
Sequence 104, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPPAE FOR
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPPAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0., Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: *MICOBACTERIUM LEPRAE*

US-08-311-731A-104

Query Match Score 36; DB 4; Length 403;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IPVLDENG 9
Db 192 VPVRDONGL 200

RESULT 37
US-09-270-767-41612
Sequence 41642, Application US/09270767
Patent No. 6703451
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
FILE REFERENCE: File Reference: 7326_094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 41642
TYPE: PRT
ORGANISM: *Drosophila melanogaster*

US-09-270-767-41642

Query Match Score 57.1%; DB 4; Length 506;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PVLDENGFLF 10
Db 110 PVVDNGVF 118

RESULT 38
US-09-543-681A-4544
Sequence 4544, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709_1002_001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIORITY FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIORITY FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO: 4544
LENGTH: 566
TYPE: PRT
ORGANISM: *Proteus mirabilis*

US-09-543-681A-4544

Query Match Score 57.1%; DB 4; Length 566;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGFLFA 11
Db 500 VPVLDAGGLHA 510

RESULT 39
US-09-252-991A-20441
Sequence 2041, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 10/196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20441
; LENGTH: 533
; TYPE: PRF
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (289), (474), (511), (523), (557) at the above locations are unknown.
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
; US-09-252-991A-20441

Query Match 57.1%; Score 36; DB 4; Length 593;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENGIFA 11
: ||| :|||
Db 491 VPADDGGIFPA 501

RESULT 40
US-09-252-991A-30731
Sequence 30731, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenstein et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 101796_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30731
LENGTH: 1428
TYPE: PRF
ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30731

Query Match 57.1%; Score 36; DB 4; Length 1428;
Best Local Similarity 72.7%; Pred. No. 6e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENGIFA 11
: ||| :|||
Db 1221 IPVLEBIGLYA 1231

Search completed: January 7, 2005, 10:06:32
Job time : 27 secs

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OM protein - protein search, using sw model 1

Run on: January 7, 2005, 10:05:37 ; Search time 469 Seconds (without alignments)

9.226 Million cell updates/sec

Title: US-09-699-224A-1

Perfect score: 63

Sequence: 1 I P V D E N G L F A P 1 1 2

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Published Applications AA:
 1: /cgn2_6_ptodata/2/pubpaas/us07_pubcomb.pep: *
 2: /cgn2_6_ptodata/2/pubpaas/pct_new_pub.pep: *
 3: /cgn2_6_ptodata/2/pubpaas/us06_new_pub.pep: *
 4: /cgn2_6_ptodata/2/pubpaas/us07_pubcomb.pep: *
 5: /cgn2_6_ptodata/2/pubpaas/us07_pubcomb.pep: *
 6: /cgn2_6_ptodata/2/pubpaas/pctus_pubcomb.pep: *
 7: /cgn2_6_ptodata/2/pubpaas/us08_pubcomb.pep: *
 8: /cgn2_6_ptodata/2/pubpaas/us09_pubcomb.pep: *
 9: /cgn2_6_ptodata/2/pubpaas/us09a_pubcomb.pep: *
 10: /cgn2_6_ptodata/2/pubpaas/us09b_pubcomb.pep: *
 11: /cgn2_6_ptodata/2/pubpaas/us09c_pubcomb.pep: *
 12: /cgn2_6_ptodata/2/pubpaas/us09_new_pub.pep: *
 13: /cgn2_6_ptodata/2/pubpaas/us09a_pubcomb.pep: *
 14: /cgn2_6_ptodata/2/pubpaas/us10b_pubcomb.pep: *
 15: /cgn2_6_ptodata/2/pubpaas/us10c_pubcomb.pep: *
 16: /cgn2_6_ptodata/2/pubpaas/us10d_pubcomb.pep: *
 17: /cgn2_6_ptodata/2/pubpaas/us10i_new_pub.pep: *
 18: /cgn2_6_ptodata/2/pubpaas/us11_new_pub.pep: *
 19: /cgn2_6_ptodata/2/pubpaas/us60_new_pub.pep: *
 20: /cgn2_6_ptodata/2/pubpaas/us60_pubcomb.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-10-424-599-220159 ; Sequence 220159, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalchuk David J

; APPLICANT: Zhou Yiliua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 18-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 220159

; LENGTH: 288

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_NRT3847_40832C.1.pep

US-10-424-599-220159 ;

Query Match 65.1%; Score 41; DB 15; Length 288;
 Best Local Similarity 77.8%; Pred. No. 68;
 Matches 7; Conservative 1; Missmatches 1; Indels 0; Gaps 0;

Qy 4 LDENGIFAP 12

| | | | : |

Db 198 LDENGIFKP 206

RESULT 2

US-10-282-122A-47568 ; Sequence 47568, Application US/10282122A

; Publication No. US20040029129A1

; Sequence 47568, Application US/10282122A ; Publication No. US20040029129A1

SUMMARIES

§

Result No.	Score	Query Match	Length	DB ID	Description
1	41	65.1	288	15 US-10-424-599-220159	Sequence 220159
2	41	65.1	691	15 US-10-282-122A-47568	Sequence 47568, A
3	41	65.1	696	15 US-10-282-122A-50917	Sequence 50917, A
4	40	63.5	200	17 US-10-424-115-39892	Sequence 339892,
5	39	61.9	280	16 US-10-437-963-114931	Sequence 114931,
6	39	61.9	316	9 US-09-738-626-3787	Sequence 5787, Ap
7	39	61.9	403	14 US-10-369-493-19334	Sequence 19334, A
8	39	61.9	688	15 US-10-282-122A-49243	Sequence 49243, A
9	39	61.9	994	16 US-10-437-963-157708	Sequence 157708,
10	39	61.9	2893	15 US-09-882-227-522	Sequence 522, App
11	39	61.9	2893	15 US-10-282-122A-58673	Sequence 58673, A
12	38	60.3	188	15 US-10-424-599-245562	Sequence 245562,
13	38	60.3	197	15 US-10-282-122A-75905	Sequence 75905, A

GENERAL INFORMATION:
 / APPLICANT: Wang, Liangsu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Pojetych, R.
 / APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: BLITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 47568
 LENGTH: 691
 TYPE: PRT
 ORGANISM: Burkholderia cepacia
 US-10-282-122A-47568

Query Match Best Local Similarity 65.1%; Score 41; DB 15; Length 691;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IPVLDENGFL 9
 Db 674 IPVLDENGFL 682

RESULT 3
 US-10-282-122A-50917
 / Sequence 50917, App1ication US/102822122A
 / GENERAL INFORMATION:
 / APPLICANT: Wang, Liangsu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Pojetych, R.
 / APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: BLITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-09-06
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 50917
 LENGTH: 696
 TYPE: PRT
 ORGANISM: Bordetella pertussis
 US-10-282-122A-50917

Query Match Best Local Similarity 65.1%; Score 41; DB 15; Length 696;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IPVLDENGFLA 11
 Db 682 VPVLDDEDGLKA 692

RESULT 4
 US-10-425-115-339892
 / Sequence 339892, Application US/10425115
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovacic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / FILE REFERENCE: 38-21(5322)B
 / CURRENT APPLICATION NUMBER: US/10/425,115
 / NUMBER OF SEQ ID NOS: 369326
 / SEQ ID NO 339892
 / LENGTH: 200
 / TYPE: PRT
 / FEATURE:
 / OTHER INFORMATION: Clone ID: MRT4577_7314C.1.pep
 / ORGANISM: Zea mays
 / APPLICANT: Carr, Grant
 / APPLICANT: Haselbeck, Robert
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Pojetych, R.
 / APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

RESULT 5
 US-10-437-963-114931
 ; Sequence 114931, Application US/10437963
 ; GENERAL INFORMATION:
 ; APPLICANT: Li Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-10(5322)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 114931
 LENGTH: 280
 TYPE: PRT
 ORGANISM: *Oryza sativa*
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(280)
 OTHER INFORMATION: unsure at all Xaa locations
 OTHER INFORMATION: Clone ID: PAT_MRT4530_18575C.1.pep
 US-10-437-963-114931

Query Match 61.9%; Score 39; DB 9; Length 316;
 Best Local Similarity 77.8%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0;
 Gaps 0;

Qy 4 LDENGLEFAP 12
 Db 167 VDENGRKFAP 175

RESULT 7
 US-10-369-493-19334
 ; Sequence 19334, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinke, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 19334
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: *Myxococcus xanthus*

Query Match 61.9%; Score 39; DB 14; Length 403;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 IPVLDENGGL 9
 Db 192 VPVVDQNGL 200

RESULT 8
 US-10-282-1122A-49243
 ; Sequence 49243, Application US/102821122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Hasselbeck, Robert
 ; APPLICANT: Ohlson, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Travick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.03A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-10
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-05-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-05-09

RESULT 6
 US-09-738-626-5787
 ; Sequence 5787, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SETKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US/09/238,626
 CURRENT FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: JP 99/377484
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: JP 00/280988
 PRIOR FILING DATE: 2000-08-03
 NUMBER OF SEQ ID NOS: 7059
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO 5787
 LENGTH: 316
 TYPE: PRT
 ORGANISM: *Corynebacterium glutamicum*
 US-09-738-626-5787

; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR APPLICATION NUMBER: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 49243
 ; LENGTH: 688
 ; TYPE: PRT
 ; ORGANISM: Burkholderia fungorum
 ; US-10-282-122A-49243

Query Match Score 61.9%; DB 15; Length 68;
 Best Local Similarity 77.8%; Pred. No. 4.1e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy	1 IPVLDENG 9	1 IPVLDENG 12
Db	672 IPVLDENG 680	2077 IPNLGKKG 1FAP 2088

RESULT 9

US-10-437-963-157708
 ; Sequence 157708, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazau, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 ; FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 157708
 ; LENGTH: 994
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_57252C.1.pep

Query Match Score 61.9%; DB 16; Length 994;
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy	3 VLDENG 12	3 VLDENG 1FAP 12
Db	395 VLMENG 404	395 VLMENG 404

RESULT 10

US-09-882-227-522
 ; Sequence 522, Application US/09882227
 ; Publication No. US20030158396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kleanthous, Harold
 ; APPLICANT: Al-Garawi, Amal
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Tomb, Jean-Francois

; APPLICANT: Oomen, Raymond P.
 ; TITLE OF INVENTION: Identification of Polynucleotides
 ; TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
 ; FILE REFERENCE: 06132/047002
 ; CURRENT APPLICATION NUMBER: US/09/882,227
 ; CURRENT FILING DATE: 2003-06-15
 ; PRIOR APPLICATION NUMBER: US 08/902,615
 ; PRIOR FILING DATE: 1997-07-29
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 522
 ; LENGTH: 2893
 ; TYPE: PRT
 ; ORGANISM: Helicobacter pylori
 ; US-09-882-227-522

Query Match Score 61.9%; DB 10;
 Best Local Similarity 66.7%; Pred. No. 2e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1 IPVLDENG 1FAP 12	1 IPVLDENG 1FAP 12
Db	2077 IPNLGKKG 1FAP 2088	2077 IPNLGKKG 1FAP 2088

RESULT 11

US-10-282-122A-58673
 ; Sequence 58673, Application US/10282122A
 ; Publication No. US2004029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlben, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELTRA.034A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 58673
 ; LENGTH: 2893
 ; TYPE: PRT

; ORGANISM: Helicobacter pylori
 US-10-282-122A-58673
 Query Match Score 39; DB 15; Length 2839;
 Best Local Similarity 61.9%; Pred. No. 2e+03;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 IPVLDENGIFAP 12
 Db 2077 IPNLGKGIFAP 2088

RESULT 12
 US-10-424-5919-245562
 ; Sequence 25562, Application US/10424599
 ; PUBLICATION NO. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 245562
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_63774C.1.pep
 US-10-424-5919-245562
 Query Match Score 38; DB 15; Length 188;
 Best Local Similarity 60.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 VLDEGLFAP 12
 Db 45 VLDEGLPVP 54

RESULT 13
 US-10-282-122A-75905
 ; Sequence 75905, Application US/10282122A
 ; PUBLICATION NO. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohleen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282-122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2003-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 48473
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48473

Query Match Similarity 60.3%; Score 38; DB 15; Length 483;
Best Local Matches 58.3%; Pred. No. 4.1e+02; Indels 0; Gaps 0; Gaps 0;
Qy 1 IPVLDENGIFAP 12
Db 343 VPVLKERRQEAVP 354

RESULT 15
US-10-260-937-14
; Sequence 14, Application US/10260937
; Publication No. US20030220305A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND METHODS OF USE
; FILE REFERENCE: 079113-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,661
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-937-14

Query Match Similarity 60.3%; Score 38; DB 14; Length 613;
Best Local Matches 58.3%; Pred. No. 5.4e+02; Indels 0; Gaps 0; Gaps 0;
Qy 1 IPVLDENGIFAP 12
Db 84 LPVLHPHGLFPRP 95

RESULT 16
US-10-156-761-9979
; Sequence 9979, Application US/10156761
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITAKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-662
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 9979
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9979

Query Match Similarity 60.3%; Score 38; DB 14; Length 707;
Best Local Matches 50.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Qy 1 IPVLDENGIFAP 12
Db 290 VPVLDDHGQMTP 301

RESULT 17
US-10-282-122A-772556
; Sequence 77256, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari
; APPLICANT: Zybikind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 7756
; LENGTH: 894
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-772556

Query Match Similarity 60.3%; Score 38; DB 15; Length 894;
Best Local Matches 100.0%; Pred. No. 8.2e+02; Indels 0; Gaps 0;
Qy 2 PVLDENG 8
Db 720 PVLDENG 726

```

RESULT 18
US-10-437-963-145171
; Sequence 15171, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Barzakuk, Brad
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 145171
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45915C.1.pep
US-10-437-963-145171
Query Match 60.3%; Score 38; DB 16; Length 1464;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 DENGFLAP 12
Db 413 DENGLIAP 420

RESULT 19
US-10-474-776-249
; Sequence 249, Application US/10474776
; Publication No. US20040110181A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAES OPEN READING FRAMES ENCODING POLYPEPTIDES
; TITLE OF INVENTION: ANTIGENS AND USES THEREOF
; FILE REFERENCE: AM10649-PCT
; CURRENT APPLICATION NUMBER: US/10/474,776
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 1659
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-474-776-249
Query Match 59.5%; Score 37.5%; DB 16; Length 1659;
Best Local Similarity 52.9%; Pred. No. 2e+03; Matches 9; Conservative 1; Mismatches 0; Indels 7; Gaps 1;

Qy 3 VLDEN-----GLFAP 12
Db 457 ILDENGKLRISIGNFAP 473

RESULT 20
US-10-014-340-737
; Sequence 737, Application US/10014340
; Publication No. US2003006441A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including

; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 737
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-737
Query Match 58.7%; Score 37; DB 14; Length 12;
Best Local Similarity 87.5%; Pred. No. 9.7%; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IPVLDENG 8
Db 3 IPVTDENG 10

RESULT 21
US-10-014-338-9
; Sequence 9, Application US/10014338
; Publication No. US20030092614A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: ADP-41, A NOVEL PROTEIN ISOLATED FROM BRAIN TISSUE HOMOGENATE AND
; FILE REFERENCE: 9195-077
; CURRENT APPLICATION NUMBER: US/10/014,338
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/014,338
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-338-9
Query Match 58.7%; Score 37; DB 14; Length 12;
Best Local Similarity 87.5%; Pred. No. 9.7%; Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IPVLDENG 8
Db 3 IPVTDENG 10

RESULT 22
US-10-460-594-97
; Sequence 97, Application US/10460594
; Publication No. US2004018979A1
; GENERAL INFORMATION:
; APPLICANT: Beachy, Philip A.,
; PORTER, Jeffrey A.
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flisch & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/460,594
 FILING DATE: 11-Jun-2003
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/061,323
 FILING DATE: 07-OCT-1997
 APPLICATION NUMBER: 08/729,743
 FILING DATE: 07-OCT-1996
 APPLICATION NUMBER: 08/567,357
 FILING DATE: 10-JUL-1996
 APPLICATION NUMBER: 08/349,498
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/140001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEX/FAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 104 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 97:
 US-10-460-594-97

Query Match 58.7%; Score 37; DB 15; Length 104;
 Best Local Similarity 72.7%; Pred. No. 1.1e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFPA 11
 Db 40 IMMLDENGILVA 50

RESULT 23
 US-10-335-977-9958
 Sequence 8958, Application US/10335977
 Publication No. US20040052799A1
 GENERAL INFORMATION:
 APPLICANT: DOUGLAS SMITH et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 RELATED TO HELICOBACTER PYLORI FOR
 DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 10031
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHTE & COCKFIELD
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: Windows NT 4.0
 SOFTWARE: UNIX
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/335,977
 FILING DATE: 30-Dec-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/993,002
 FILING DATE: 17-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEX/FAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 8958:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Helicobacter pylori
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...105
 SEQUENCE DESCRIPTION: SEQ ID NO: 8958:
 US-10-335-977-9958

Query Match 58.7%; Score 37; DB 15; Length 105;
 Best Local Similarity 58.3%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFPA 12
 Db 14 IPVNGKKGIFAP 25

RESULT 24
 US-10-425-114-39021
 Sequence 39021, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 39021
 LENGTH: 136
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3158-010-D7_FLI.pep
 US-10-425-114-39021

Query Match 58.7%; Score 37; DB 15; Length 136;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IPVLDENGIFPA 12
 Db 89 IPVYDGGAKAP 100

RESULT 25
 US-09-903-456-40
 Sequence 40, Application US/09903456
 Publication No. US20020138874A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Leonard, Amanda Run-Young
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
 FILE REFERENCE: 6407.US.P3
 CURRENT APPLICATION NUMBER: US/09/903,456
 CURRENT FILING DATE: 2001-07-11
 PRIOR APPLICATION NUMBER: US 09/624,670

```

; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 40
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
; SEQ ID NO: 456-40
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1998-08-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 81
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
; SEQ ID NO: 37
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
US-10-408-736-37
Query Match      58.7%; Score 37; DB 9; Length 174;
Best Local Similarity 60.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; 2; Indels 0; Gaps 0;
Qy   1 IPVLDENGFL 10
Db   80 VPILLARNGLF 89

RESULT 26
US-10-156-911-40
; Sequence 40, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Young
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US/09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US/09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 40
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
; SEQ ID NO: 911-40
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407 US P1
; CURRENT APPLICATION NUMBER: US/10/408,736
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/379,095A
; PRIOR FILING DATE: 1998-08-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 81
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
; SEQ ID NO: 37
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Mortierella alpina
US-10-156-911-40
Query Match      58.7%; Score 37; DB 14; Length 174;
Best Local Similarity 60.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2; 2; Indels 0; Gaps 0;
Qy   1 IPVLDENGFL 10
Db   80 VPILLARNGLF 89

RESULT 27
US-10-408-736-37
; Sequence 37, Application US/10408736
; Publication No. US20030177508A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Das, Tapas
; APPLICANT: Parker-Barnes, Jennifer M.
; APPLICANT: Leonard, Amanda Eun-Young
; APPLICANT: Thurmond, Jennifer M.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1113 PCT
; CURRENT APPLICATION NUMBER: US/10/220,120
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/184,778; 60/184,797; 60/184,698; 60/184,770; 60/184,774;
; APPLICANT: JACKSON, Stuart
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wenshang
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: COHEN, Wenshang
; APPLICANT: JACKSON, Stuart
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAPFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wenshang
; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: COHEN, Wenshang
; APPLICANT: JACKSON, Stuart
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1113 PCT
; CURRENT APPLICATION NUMBER: US/10/220,120
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/184,693; 60/184,771; 60/184,773; 60/184,776;
; APPLICANT: 60/184,769; 60/184,768; 60/184,837; 60/184,697; 60/184,841;
; APPLICANT: 60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/205,221;

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Query Match
Best Local Similarity 58.7%; Score 37; DB 15; Length 174;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IPVLDENG 8
Db 104 IPVTDENG 111

RESULT 29
US-09-903-456-26
Sequence 26, Application US/09903456
Patent No. US002013887A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 393
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:978427.5.orf2:2000FEB18
FEATURE:
NAME/KEY: unsure
LOCATION: 151
OTHER INFORMATION: unknown or other
US-10-220-120-393

Query Match
Best Local Similarity 87.5%; Score 37; DB 15; Length 174;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IPVLDENG 8
Db 104 IPVTDENG 111

RESULT 30
US-10-156-911-26
Sequence 26, Application US/10156911
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P4
CURRENT APPLICATION NUMBER: US/10/156,911
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/903,456
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 178
TYPE: PRT
ORGANISM: Mortierella alpina
US-10-156-911-26

Query Match
Best Local Similarity 60.0%; Score 37; DB 9; Length 178;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENG 10
Db 3 VPILARGLF 12

RESULT 31
US-10-408-736-23
Sequence 23, Application US/10408736
Publication No. US20030177508A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Dab, Tapas
APPLICANT: Huang, Yung-Sheng
APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Thurnmond, Jennifer M.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P1
CURRENT APPLICATION NUMBER: US/10/408,736
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US/09/379,095A
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 178
TYPE: PRT
ORGANISM: Mortierella alpina
US-10-408-736-23

Query Match
Best Local Similarity 58.7%; Score 37; DB 14; Length 178;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENG 10
Db 3 VPILARGLF 12

RESULT 30
US-10-156-911-26

RESULT 32
US-10-767-701-33319
Sequence 33319, Application US-10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 8-21(53535)B
CURRENT APPLICATION NUMBER: US-10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS:
SEQ ID NO 33319
LENGTH: 180
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C29522_1.pep
US-10-767-701-33319
Query Match 58.7%; Score 37; DB 16; Length 180;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
RESULT 33
US-10-220-481-9
Sequence 9, Application US-10220481
Publication No. US20040110670A1
GENERAL INFORMATION:
APPLICANT: ARICO, Maria B., et al.
TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/01US
CURRENT APPLICATION NUMBER: US-10/220,481
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 633
SEQ ID NO 9
LENGTH: 196
TYPE: PRT
ORGANISM: Escherichia coli
US-10-220-481-9
Query Match 58.7%; Score 37; DB 16; Length 196;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RESULT 34
US-09-903-456-38
Sequence 38, Application US-09903456
Patent No. US20020138874A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3

CURRENT APPLICATION NUMBER: US-09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US-09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US-09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US-09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 219
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-903-456-38
Query Match 58.7%; Score 37; DB 9; Length 219;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RESULT 35
US-10-156-911-38
Sequence 38, Application US-10156911
Publication No. US20030163845A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P4
CURRENT APPLICATION NUMBER: US-10/156,911
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US-09/903,456
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US-09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US-09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US-09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 219
TYPE: PRT
ORGANISM: Mortierella alpina
US-10-156-911-38
Query Match 58.7%; Score 37; DB 14; Length 219;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RESULT 36
US-10-408-736-35
Sequence 35, Application US-10408736
Publication No. US2003017750BA1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Young
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3

```

; APPLICANT: Parker-Barnes, Jennifer M. ; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: Leonard, Amanda Eun-Young ; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: Thurmond, Jennifer M. ; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: 6407.US.P1 ; FILE REFERENCE: Related Diseases
; CURRENT APPLICATION NUMBER: US/10/408,736 ; FILE REFERENCE: P1948R1.US
; CURRENT FILING DATE: 2003-04-04 ; CURRENT APPLICATION NUMBER: US/10/370,715B
; PRIOR APPLICATION NUMBER: US/09/379,095A ; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-08-23 ; NUMBER OF SEQ ID NOS: 742
; NUMBER OF SEQ ID NOS: 8 ; SEQ ID NO: 146
; SOFTWARE: FastSEQ for Windows Version 4.0 ; LENGTH: 236
; SEQ ID NO: 35 ; TYPE: PRT
; LENGTH: 219 ; ORGANISM: Mortierella alpina
; TYPE: PRT ; US-10-408-736-35
; ORGANISM: Mortierella alpina ; Score 37; DB 14; Length 219;
; Best Local Similarity 60.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Query Match ; Matches 2; Mismatches 2;保守型 0; Gaps 0;
Qy 1 IPVLDENG 10
Db 1.0 VPILANGLF 19
; RESULT 39
; US-09-903-456-28
; Sequence 28, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Young
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Surette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 28
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (280) ; (280)
; OTHER INFORMATION: Xaa = Unknown or Other at position 280
; US-09-903-456-28
; Query Match
; Best Local Similarity 60.0%; Pred. No. 3.3e+02; Mismatches 2;保守型 0; Gaps 0;
Query Match ; Matches 6; Mismatches 2;保守型 0; Gaps 0;
Qy 1 IPVLDENG 10
Db 1.19 VPILANGLF 79
; RESULT 40
; US-10-156-911-28
; Sequence 28, Application US/10156911
; PUBLICATION NO. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Young
; APPLICANT: Clark, Hillary
; APPLICANT: Botsdell, Hunt
; APPLICANT: Jackman, Janet
; APPLICANT: Schoenfeld, Jill R.

; APPLICANT: Parker-Barnes, Jennifer M. ; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: Leonard, Amanda Eun-Young ; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: Thurmond, Jennifer M. ; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: 6407.US.P1 ; FILE REFERENCE: Related Diseases
; CURRENT APPLICATION NUMBER: US/10/408,736 ; FILE REFERENCE: P1948R1.US
; CURRENT FILING DATE: 2003-04-04 ; CURRENT APPLICATION NUMBER: US/10/370,715B
; PRIOR APPLICATION NUMBER: US/09/379,095A ; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-08-23 ; NUMBER OF SEQ ID NOS: 742
; NUMBER OF SEQ ID NOS: 8 ; SEQ ID NO: 146
; SOFTWARE: FastSEQ for Windows Version 4.0 ; LENGTH: 236
; SEQ ID NO: 35 ; TYPE: PRT
; LENGTH: 219 ; ORGANISM: Mortierella alpina
; TYPE: PRT ; US-10-408-736-35
; ORGANISM: Mortierella alpina ; Score 37; DB 16; Length 236;
; Best Local Similarity 87.5%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Query Match ; Matches 7; Mismatches 0;保守型 0; Gaps 0;
Qy 1 IPVLDENG 8
Db 1.19 IPVTDENG 126
; RESULT 38
; US-10-370-715B-146
; Sequence 146, Application US/10370715B
; PUBLICATION NO. US20020258678A1
; GENERAL INFORMATION:
; PATIN Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BOTSDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.

```

APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P4
CURRENT APPLICATION NUMBER: US/10/156,911
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 09/903,456
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 28
LENGTH: 280
TYPE: PRT
ORGANISM: Mortierella alpina
FEATURE:
NAME/KEY: VARIANT
LOCATION: (280)..
OTHER INFORMATION: Xaa = Unknown or Other at position 280
US-10-156-911-28

Query Match 58.7%; Score 37; DB 14; Length 280;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IPVLDENGIF 10
Db :|||
Db 70 VPILARNGIF 79

Search completed: January 7, 2005, 10:19:19
Job time : 470 secs

je Blank (uspij)

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OM protein - protein search, using sw model

Run on: January 7, 2005, 10:02:01 ; Search time 25 Seconds
(without alignments)

Title: US-09-699-224A-1

Perfect score: 63

Sequence: 1 IPVLDENGFLPAP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡ Maximum Match 100‡ Listing first 45 summaries

Database : PIR_79;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	71.4	359	C84983	hypothetical prote
2	41	65.1	180	T35196	hypothetical prote
3	41	65.1	707	F69185	probable DNA gyras
4	40	63.5	157	AF2724	YhcY homolog MTH64
5	40	63.5	337	B97506	hypothetical prote
6	40	63.5	337	H97350	peptide ABC transp
7	39	61.9	140	AC0929	two CBS domain con
8	39	61.9	450	G75318	nitritotriacetate
9	39	61.9	700	S64951	DNA ligase - Dein
10	39	61.9	764	A82255	hypothetical prote
11	39	61.9	1621	A64556	hypothetical prote
12	39	61.9	2893	T08505	toxin-like outer m
13	38	60.3	162	E97298	triflB protein - Ent
14	38	60.3	197	RGBYC3	hypothetical prote
15	38	60.3	197	A90664	unknown protein fr
16	38	60.3	197	F88514	flagellar hook-bas
17	38	60.3	268	G69623	uncharacterized Fe
18	38	60.3	298	E97298	regulatory protein
19	38	60.3	322	AF0864	membrane-bound lyt
20	38	60.3	365	D84618	probable amino aci
21	38	60.3	620	E82221	DNA gyrase, chain
22	38	60.3	894	G95057	endo-beta-N-acetyl
23	37.5	59.5	1659	F83988	hypothetical prote
24	37.5	59.5	1659	H97926	inosine-2'-monopho
25	37	58.7	144	AB0982	probable 2-hydroxy
26	37	58.7	324	C65154	probable 2-hydroxy
27	37	58.7	328	F91183	probable dehydroge
28	37	58.7	328	B86030	probable dehydroge
29	37	58.7	1051	C95367	conserved hypothet

ALIGNMENTS

RESULT 1						
C84983	hypothetical protein mlta [imported] - Buchnera sp.					
C;Species: Buchnera sp.						
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001						
C;Accession: C84983						
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakai, Y.; Ishikawa, H.	Nature 407, 81-86, 2000					
A;Title: Genome sequence of the endosymbiotic bacterial symbiont of aphids Buchnera sp. A						
A;Reference number: A84930; PMID:20445173; PMID:10993077						
A;Accession: C84983						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-359 <STO>						
A;Cross-references: GB:AP000398; GSPDB:GN00144						
A;Experimental source: Strain APS						
C;Genetics:						
A;Gene: mlta; BU458						
Query Match	71.4%	Score 45;	DB 2;	Length 359;		
Best Local Similarity	70.0%	Pred. No. 2.1;				
Matches 7;	Conservative	3; Mismatches	0;	Indels 0;	Gaps 0;	
QY	1 IPVLDENGFLP 10					
Db	298 IPVLDENGVP 307					
RESULT 2						
A98321	hypothetical 15.0K protein in coba 3' region (orf6) [imported] - Agrobacterium tumefaciens					
C;Species: Agrobacterium tumefaciens						
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004						
C;Accession: A98321						
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Quroollo, M.; Goldman, B.; Liu, F.; Wollam, C.; Altinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Sciente 294, 2323-2328, 2001	A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum					
A;Reference number: A97359; PMID:21608551; PMID:11743194	A;Accession: A98321					
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-180 <KUR>						
A;Cross-references: UNIPROT:Q8UAS1; GB:AE007870; PIDN:AAK90091.1; PMID:915160078; GSDB:G	C;Genetics:					
A;Gene: AGR_L_3039	C;Superfamily: Transporter DME family					
Query Match	65.1%	Score 41;	DB 2;	Length 180;		
Best Local Similarity	50.0%	Pred. No. 5.2;				
Matches 6;	Conservative	3; Mismatches	3;	Indels 0;	Gaps 0;	

erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; KarP, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001.

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, R.; Seeger, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2777; MUID:21608850; PMID:11743193

A;Accession: AF2724

A;Status: preliminary

C;Species: Streptomyces coelicolor

C;Accession: T35196

C;Cross-references: UNIPROT:Q8UG41; GB:AE008688; PIDN:AAL42212.1; PIDN:g17739605; GSPDB:G

R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, April 1998

A;Reference number: Z21571

A;Accession: T35196

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-707 <SSE>

A;Cross-references: UNIPROT:O63998; EMBL:AL022374; PIDN:CAA18520.1; GSPDB:GN00070; SCOED

A;Experimental source: strain A3 (2)

C;Genetics:

A;Gene: ynrB; SCOEDB:SC5BB.12

C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match Score 65.1% Best Local Similarity 58.3% Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 290 VPIVDENGFLFAP 301

RESULT 6

Query Match Score 41; Best Local Similarity 58.2% Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 290 VPIVDENGFLFAP 12

peptide ABC transporter, ATP-binding protein [imported] - Agrobacterium tumefaciens (str

C;Species: Agrobacterium tumefaciens

C;Accession: B97506

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Liu, F.; Wollam, C.; Doughty, D.; Scott, C.; Lappas, C.; Markez, B.; Science 294, 2323-2328, 2001.

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: B97506

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <KUR>

A;Cross-references: UNIPROT:Q8UG41; GB:AE007869; PIDN:AAK87003.1; PIDN:g15156245; GSPDB:G

C;Genetics:

A;Gene: AGR C 2214

A;Map position: circular chromosome

Query Match Score 63.5% Best Local Similarity 70.0% Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 272 MLDEDTGLYAP 281

RESULT 7

Query Match Score 40; Best Local Similarity 63.6% Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 133 IPIVIDENGRIA 143

two CBS domain containing protein [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: H97350

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 <KUR>

A;Cross-references: UNIPROT:Q97D09; GB:AB001477; PIDN:AXX81595.1; PIDN:g15026776; GSPDB:G

R;Nodd, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

C;Genetics:

A;Gene: CAC3674	Query Match 61.9%; Score 39; DB 2; Length 140; Best Local Similarity 60.0%; Pred. No. 9.1.; Indels 0; Gaps 0;	Db 661 VPVLDEGLAA 671
Qy 1 IPVLDENGIF 10	RESULT 10 S64951 hypothetical protein YLR114C - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein L2941 C;Species: Saccharomyces cerevisiae C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004 C;Accession: S64951; S69401 R;Verhaaselt, P.; Vet, M.; Volckaert, G. submitted to the Protein Sequence Database, May 1996 A;Reference number: S64943 A;Accession: S64951 A;Molecule type: DNA A;Residues: 1-764 <VER> A;Cross-references: UNIPROT:O12500; EMBL:Z73286; NID:91360509; PIDN:CAA97681-1; PID:e245 A;Experimental source: strain S288C A;Submitted to the EMBL Data Library, September 1995 A;Reference number: S69393 A;Accession: S69401 A;Molecule type: DNA A;Residues: 1-764 <NEW> A;Cross-references: EMBL:X89514; NID:91297019; PIDN:CAA61692-1; PID:e198747; PID:9129702	
Db 37 IPILDDNGKRY 46	AB3238 nitrotriacetate monooxygenase, component A Atu6084 [Imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens C:Accession: AB3238 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C:Residues: 1-450 <KUR> A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Status: preliminary A;Molecule type: DNA A;Cross-references: UNIPROT:Q8U651; GB:AE008690; PIDN:AAI46320-1; PID:917744106; GSDB:G A;Experimental source: strain C58 (Dupont) C;Genetics: A;Gene: Atu6084 A;Genome: plasmid C;Supertaxonomy: nitrilotriacetate monooxygenase	
Qy 1 IPVLDENGIF 10	Query Match 61.9%; Score 39; DB 2; Length 450; Best Local Similarity 70.0%; Pred. No. 34; Indels 0; Gaps 0;	Db 406 VPVLQERGLIF 415
Db	RESULT 11 A82255 hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Accession: A82255 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1621 <HEI> A;Cross-references: UNIPROT:Q9KTAS; GB:AE004181; GB:AE003852; NID:g9655454; PIDN:AAF9415 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC0998 A;Map position: 1	Query Match 61.9%; Score 39; DB 2; Length 1621; Best Local Similarity 80.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Qy 2 PVLDENGIF 11	RESULT 12 A82255 hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Accession: A82255 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1621 <HEI> A;Cross-references: UNIPROT:Q9KTAS; GB:AE004181; GB:AE003852; NID:g9655454; PIDN:AAF9415 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC0998 A;Map position: 1	Query Match 61.9%; Score 39; DB 2; Length 1621; Best Local Similarity 80.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Db 743 PVLDENEAFKA 752	RESULT 13 A82255 hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Accession: A82255 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1621 <HEI> A;Cross-references: UNIPROT:Q9KTAS; GB:AE004181; GB:AE003852; NID:g9655454; PIDN:AAF9415 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VC0998 A;Map position: 1	Query Match 61.9%; Score 39; DB 2; Length 1621; Best Local Similarity 80.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Qy 1 IPVLDENGIFLA 11	RESULT 14 A82255 hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Accession: A82255 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1700 <WHI> A;Cross-references: UNIPROT:Q9RSQ5; GB:AE002043; GB:AE000513; NID:g6459859; PIDN:AAF1161 A;Experimental source: strain R1 C;Genetics: A;Gene: DR2069 A;Superfamily: NAD+-dependent DNA ligase, liga type	Query Match 61.9%; Score 39; DB 2; Length 700; Best Local Similarity 72.7%; Pred. No. 57; Indels 0; Gaps 0;
Db	RESULT 15 A82255 hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C;Species: Vibrio cholerae C;Accession: A82255 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brinkac, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: G75318 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-700 <WHI> A;Cross-references: UNIPROT:Q9RSQ5; GB:AE002043; GB:AE000513; NID:g6459859; PIDN:AAF1161 A;Experimental source: strain R1 C;Genetics: A;Gene: DR2069 A;Superfamily: NAD+-dependent DNA ligase, liga type	Query Match 61.9%; Score 39; DB 2; Length 700; Best Local Similarity 80.0%; Pred. No. 57; Indels 0; Gaps 0;

toxin-like outer membrane protein HP0289 - *Helicobacter pylori* (strain 26695)
 C;Species: *Helicobacter pylori*
 C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C;Accession: A64556
 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mclennan,
 Bon, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.
 A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A;Reference number: A64520; MUID:97394467; PMID:92552185
 A;Accession: A64556
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-2893 <TOM>
 A;Cross-references: UNIPROT:O25063; GB:AB000547; GB:ABE000511; NID:g23133777; PIDN:AAD0735

Query Match 61.9%; Score 39; DB 2; Length 2893;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 PVLDEGLFAP 12
 Db 2077 IPNLGKKGCFAP 2088

RESULT 13
 TO8505

trbH protein - *Enterobacter aerogenes* plasmid R751.
 C;Species: *Enterobacter aerogenes*
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: TO8505
 R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
 Plasmid 36, 95-111, 1996
 A;Title: Conservation of the genetic switch between replication and transfer genes of In
 A;Reference number: Z16434; MUID:97118926; PMID:8954881
 A;Accession: TO8505
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-162 <TMO>
 A;Cross-references: UNIPROT:P71183; EMBL:U67194; NID:g1572520; PIDN: AAC64449.1; PID:9157

A;Gene: tRNA
 A;Genome: plasmid R751

Query Match 60.3%; Score 38; DB 2; Length 162;

Best Local Similarity 63.6%; Pred. No. 16;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PVLDEGLFAP 12
 Db 144 PYLAQNGTFAP 154

RESULT 14
 AC0929

hypothetical protein STRY3692 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi
 C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 C;Note: this species has also been called *Salmonella typhi*

C;Accession: AC0929
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A;Reference number: AB0502; MUID:21534947; PMID:11671608
 A;Accession: AC0929
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-197 <PAR>

A;Cross-references: GB:AL513382; PIDN: CAD09453.1; PID: g16504570; GSPDB:GN00176

C;Genetics:
 C;Gene: SRY3692
 C;Superfamily: phage T4 tail fiber assembly protein gp38

Query Match 60.3%; Score 38; DB 2; Length 197;
 Best Local Similarity 87.5%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PVLDEGL 9
 Db 3 PVFDENG 1.0

RESULT 15
 A90664

hypothetical protein EC0281 [imported] - *Escherichia coli* (strain O157:H7, substrate RI
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: A90664
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:1258796
 A;Accession: A90664

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-197 <HAY>

A;Cross-references: UNIPROT:Q8X7M0; GB:BA000007; PIDN:BAB33704.1; PID: g13359738; GSPDB:G
 A;Experimental source: strain O157:H7, substrate RIMD 0509952
 C;Genetics:
 C;Gene: EC0281

Query Match 60.3%; Score 38; DB 2; Length 197;
 Best Local Similarity 87.5%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PVLDEGL 9
 Db 3 PVFDENG 1.0

RESULT 16
 F85514

unknown protein from prophage CP-933H [imported] - *Escherichia coli* (strain O157:H7, sub
 C;Species: *Escherichia coli*
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: F85514
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Gröbbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca,
 Niture 40, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:12106551
 A;Accession: F85514

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-197 <STO>

A;Cross-references: UNIPROT:Q8X7M0; GB:AE005174; NID:g12513030; PIDN:AGG54578.1; GSPDB:G
 A;Experimental source: strain O157:H7, substrate EDL933
 C;Genetics:
 C;Gene: 20316

Query Match 60.3%; Score 38; DB 2; Length 197;
 Best Local Similarity 87.5%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PVLDEGL 9
 Db 3 PVFDENG 1.0

' S.; Moule, S.; O'Gaura, P.
 Nature 413, 948-852, 2001
 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skalton, J.; Stevens, K.;
 A; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A; Reference number: AB0502; MUID:21534947; PMID:11677608
 A; Accession: AF0864
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-365 <PAR>
 A; Cross-references: GB:AL513382; PIDN:CADD2814.1; PID:gi16504068; GSPDB:GN00176
 A; Gene: STY3128

Query Match 60.3%; Score 38; DB 2; Length 365;
 Best Local Similarity 54.5%; Prod. No. 41;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGGLFPA 11
 Db 295 VPVLDDNNKFS 305

RESULT 21

DE4618
 Probable amino acid acetyltransferase [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Aug-2004
 C;Accession: D84618
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, L.; Talon, L.;
 Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.;
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:1061797
 A;Accession: DB4618
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-620 <STO>
 A; Cross-references: GB:AE002093; NID:gi3445208; PIDN: AAC32438.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At5g22910
 A;Map position: 2
 C;Superfamily: Amino-acid N-acetyltransferase with amino acid kinase domain

Query Match 60.3%; Score 38; DB 2; Length 620;
 Best Local Similarity 100.0%; Prod. No. 75;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLDENG 8
 Db 300 PVLDENG 306

RESULT 22

E82221
 DNA gyrase, chain A VC1258 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Accession: E82221
 R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 J.; Charlsden, D.; Brumfitt, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragot, I.; Sellers, E.;
 Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:10953301
 A;Accession: E82221
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-894 <HEI>
 A; Cross-references: UNIPROT:Q9KSJ8; GB:AE004205; PIDN: AAC99244.1; PID:gi1548007; GSPDB:G.
 C;Genetics:
 A;Gene: VC1258

RESULT 25
F83988
 inosine-5'-monophosphate dehydrogenase BH2710 [imported] - *Bacillus halodurans* (strain C)
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: F83988
 R;Rakami, H.; Nakasone, K.; Takaii, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and
 A;Reference number: A81650; MUID:1105132
 A;Accession: F83988
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-144 <STO>
 A;Cross-references: UNIPROT:Q9K9D8; GB:AP001516; GB:BA000004; NID:910175192; PIDN:BAB064
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2710

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Matches	Indels	Gaps
Qy 1 IPVLDENGIF 10	58.7%	2	144	50.0%	22	0	4	1	0
Db 106 VPVYDDGIGF 115									

RESULT 26
AB0982
 probable 2-hydroxyacid dehydrogenase STY4156 [imported] - *Salmonella enterica* subsp. ent.
 C;Species: *Salmonella enterica* subsp. enterica serovar Typhi
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0982
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 S.; T.; Connerton, P.; Cronin, A.; Davies, P.; Dowd, L.; White, N.; Farrar,
Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0982
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-324 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD07982-1; PID:gi16504968; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY4156
 C;Superfamily: phosphoglycerate dehydrogenase

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Matches	Indels	Gaps
Qy 2 PVLDENGIF 11	58.7%	2	324	70.0%	55	0	1	2	0
Db 239 PVDENALIA 248									

RESULT 27
C61154
 probable 2-hydroxyacid dehydrogenase in bigC-cBPA intergenic region - *Escherichia coli* O35
 C;Species: hypothetical protein O35
 C;Species: *Escherichia coli*
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C;Accession: C61154; S4774
 R;Plattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perra, N.T.; Burland, V.; Riley, M.; Co
 A;Rose, D.J.; Mau, B.; Shao, Y.
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: C61514

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-328 <BLAT>
 A;Cross-references: GB:AE000432; GB:000096; NID:92367241; PIDN: AAC76577-1; PID:92367243;
 A;Experimental source: strain K-12, substrate MG1655
 R;Plunkett, G.
 submitted to the EMBL Data Library, March 1994
 A;Reference number: S47666
 A;Accession: S47774
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-327 'TKPRLRRVKPDNRSGFYSLUGCSNCSPGLIKMLCR' <PLU>
 A;Cross-references: EMBL:U00139; NID:9466582; PIDN: AAB18530-1; PID:9466691
 A;Note: this sequence has been corrected
 C;Genetics:
 A;Gene: YiaE
 C;Superfamily: phosphoglycerate dehydrogenase
 Query Match Score DB Length Best Local Similarity Pred. No. Matches 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 7; Score 58.7%; DB 2; Length 328;
 Qy 2 PVLDENGIF 11
 Db 243 PVDENALIA 252

RESULT 28
F91183
 probable dehydrogenase [imported] - *Escherichia coli* (strain O157:H7, substrate RIMD 050
 C;Species: *Escherichia coli*
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;Accession: F91183
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Sasayawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: F91183
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-328 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BAB37861-1; PID:gi13363912; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrate RIMD 050952
 C;Genetics:
 A;Gene: ECg438
 C;Superfamily: phosphoglycerate dehydrogenase
 Query Match Score DB Length Best Local Similarity Pred. No. Matches 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 7; Score 58.7%; DB 2; Length 328;
 Qy 2 PVLDENGIF 11
 Db 243 PVDENALIA 252

RESULT 29
B86030
 probable dehydrogenase YiaE [imported] - *Escherichia coli* (strain O157:H7, substrate EDL
 C;Species: *Escherichia coli*
 C;Accession: B86030
 R;Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: B86030
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-328 <STO>
 A;Cross-references: GB:AE005174; PIDN:AAG58702-1; GSPDB:GN00145; UWGP:Z49

A;Experimental source: strain O157:H7, substrate EDL933
C;Genetics:

C;Superfamily: phosphoglycerate dehydrogenase

Query Match 58.7%; Score 37; DB 2; Length 328;
Best Local Similarity 70.0%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 2;
Indels 0; Gaps 0;

Qy 2 PVDENGIFPA 11
Db 243 PVDENALIA 252

RESULT 30

translation initiation factor IF-2B alpha chain [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2251
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB11807; MUID:21595285; PMID:11759840
A;Accession: AG2251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <KUR>
A;Cross-references: UNIPROT:QBYR82; GB:BA000019; PIDN:BAB75265_1; PID:91132699; GSPDB:G

A;Experimental source: strain PCC 7120
C;Genetics:

C;Superfamily: translation initiation factor eIF-2B

Query Match 58.7%; Score 37; DB 2; Length 347;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 2;
Indels 0; Gaps 0;

RESULT 31

tricarboxylate carrier - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C;Accession: 155210
R;Azzi, A.; Gierer, M.; Koller, R.; Martens, W.; Spycher, S.
J. Bioenerg. Biomembr. 25, 515-524, 1993
A;Title: The mitochondrial tricarboxylate carrier.
A;Reference number: 155210; MUID:9417933; PMID:8132491
A;Accession: 155210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-157 <RES>
A;Cross-references: GB:S70011; PIDN:ABB10258_1; PID:9545998

C;Superfamily: Saccharomyces probable membrane protein YOR271c

Query Match 58.7%; Score 37; DB 2; Length 357;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 32

Query 1 IPVLDENGIF 12
Db 326 ITTENGAFAP 335

RESULT 33

membrane-bound lytic murein transglycosylase A (EC 3.2.1.-) precursor - Escherichia coli

C;Species: Escherichia coli
C;Accession: A65064
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:974661_7; PMID:9278503

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-365 <BLAT>

A;Cross-references: UNIPROT:P46885; GB:AE000165; GB:U00096; NID:92367163; PIDN:AAAC75855.

RESULT 32

Db 240 IPVLDENG 247

RESULT 33

membrane-bound lytic murein transglycosylase A (EC 3.2.1.-) precursor - Escherichia coli

C;Species: Escherichia coli
C;Accession: C85933
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, J.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, M.; Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:2107935; PMID:11205551
A;Accession: C85933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STO>
A;Cross-references: UNIPROT:P46885; GB:AE005174; NID:912517295; PIDN:AAG57927_1; GSPDB:GI
A;Experimental source: strain O157:H7, substrate EDL933
C;Genetics:
A;Gene: mta

Query Match 58.7%; Score 37; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IPVLDENGIF 10
Db 295 VPVLDDNGKF 304

RESULT 34

membrane-bound lytic murein transglycosylase A (EC 3.2.1.-) precursor - Escherichia coli

C;Species: Escherichia coli
C;Accession: A65064
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:974661_7; PMID:9278503

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-365 <BLAT>

A;Cross-references: UNIPROT:P46885; GB:AE000165; GB:U00096; NID:92367163; PIDN:AAAC75855.

A;Experimental source: strain K-12, substrate MG1655

A;Accession: S38327
A;Molecule type: mRNA
A;Residues: 1-443 <MR>
A;Cross-references: UNIPROT:P43394; EMBL:L07249; NID:gi16810; PID:gi1668
R;Bevan, M.; Pohl, T.; Weizenecker, T.; Bancroft, I.; Mayer, H.W.; Newes, K.F.X.; Lemcke
Submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16991
A;Accession: T10204
A;Molecule type: DNA
A;Residues: 1-65, N, 67-443 <BEV>
A;Cross-references: EMBL:Alu079349; GSPDB:GN00062; ATSP:P25G13.110
A;Experimental source: Cultivar Columbia; BAC clone F25G13
C;Genetics:
A;Gene: MHK; ATSP:F25G13.110
A;Map position: 4
A;Introns: 37/3; 60/3; 137/1; 171/2; 189/1; 211/2; 247/3; 269/3; 292/3; 312/1; 347
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P10-267/Domain: protein kinase homology <KIN>
F18-26/Region: protein kinase ATP-binding motif

Query Match 58.7%; Score 37; DB 2; Length 443;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DENGFLFAP 12
Db 382 DENGFLHAP 389

RESULT 40
T19628
hypothetical protein C32A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Thomas, K.
Submitted to the EMBL Data Library, February 1995
A;Reference number: Z19154
A;Accession: T19628
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-468 <WIL>
A;Cross-references: UNIPROT:Q09260; EMBL:Z48241; PIDN:CAA88284.1; GSPDB:GN00021; CE3P:CG
C;Genetics:
A;Gene: C32A3.1
A;Map position: 3
A;Introns: 33/2; 155/3; 261/3; 409/2

Query Match 58.7%; Score 37; DB 2; Length 468;
Best Local Similarity 54.5%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PVLDENGFLFAP 12
Db 238 PIVDENNLAVP 248

Search completed: January 7, 2005, 10:06:00
Job time : 27 secs

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5				
Searched:	1825181 seqs, 575374646 residues					
Total number of hits satisfying chosen parameters:	1825181					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing: Minimum Match 0%	Maximum Match 100%					
Database :	UniProt 02.*	Listing first 45 summaries				
	1: uniprot_sprot:*					
	2: uniprot_trembl:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Match	Length	DB	ID
- - -	- - -	- - -	- - -	- - -	- - -	- - -
1	46	73.0	332	2	Q96255	
2	46	73.0	366	1	MLTA_BUCA1	
3	45	71.4	359	1	MLTA_BUCA1	
4	43	68.3	136	2	Q8XIG7	
5	43	68.3	955	2	Q8YVU0	
6	42	66.7	942	2	Q6S734	
7	42	66.7	942	2	AAS55735	
8	42	66.7	1058	2	Q6XPT1	
9	42	66.7	1058	2	CAE75591	
10	42	66.7	1058	2	CAF46169	
11	42	66.7	1576	2	Q8CM69	
12	41	65.1	180	2	Q7CS40	
13	41	65.1	209	2	Q6XIF9	
14	41	65.1	209	2	AAR09894	
15	41	65.1	245	2	O31394	
16	41	65.1	320	2	Q6FMK9	
17	41	65.1	521	2	Q728L3	
18	41	65.1	521	2	AAS97062	
19	41	65.1	696	2	Q7VRX7	
20	41	65.1	696	2	Q7WOT4	
21	41	65.1	696	2	Q7WCJ7	
22	41	65.1	702	2	Q83VW6	
23	41	65.1	702	2	Q83WB8	
24	41	65.1	707	2	Q69998	
25	41	65.1	778	2	Q6CPB9	
26	41	65.1	2255	2	Q71TF8	
27	41	65.1	2255	2	AAQ13985	
28	41	65.1	2255	2	AAQ14093	
29	41	65.1	2462	2	Q8RGZ3	
30	41	65.1	2806	2	Q8RI19	
31	41	65.1	3119	2	Q7P6S5	

ALIGNMENTS

Run on:	January 7, 2005, 10:01:57 ; Search time 108 Seconds (without alignments)			
Title:	US-09-699-224A-1			
Perfect score:	63			
Sequence:	1 IPVTDENGULFAP 12			
Scoring table:	BLOSUM62			
Seared:	1825181 seqs, 575374646 residues			
RESULT 1				
Q96255	PRELIMINARY ;			
ID Q96255;				
AC Q96255;				
DT 01-DEC-2001 (TREMBLrel. 19, Created)				
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE Hypothetical protein SR1760.				
GN OrderedLocusNames=ST1760.				
OS Sulfolobus tokodaii.				
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;				
OC Sulfolobus.				
OX NCBI_TaxID=111955;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=JCM 10545 / 7;				
RX MEDLINE=21456156; PubMed=11572479;				
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Hosoyama A., Fukui S., Sekine M., Baba S.-I., Ankai A., Kosugi H., Nakazawa H., Takanishi M., Kato O Y., Nagai Y., Nishijima K., Otsuka R., Nakazawa T., Tanaka T., Kudo Y., Yamada S., Nishimura M., Yamagishi A., Yoshizawa T., Aoki K.-I., Masuda S., Oghuchi H., Oshima T., Kikuchi H;				
RA Aoki K.-I., Masuda S., Nishimura M., Yamagishi A., Oshima T., Kikuchi H;				
RT Crearchaeon, Sulfolobus tokodaii strain7.;				
DR EMBL; AP00198; BAB66848.1. -.				
KW Complete genome of an aerobic thermoacidophilic				
SQ SEQUENCE 332 AA; MW: 38801 MW; ACAD1F64C3APEAA9 CRC64;				
Query Match				
Best Local Similarity 73.0% ; Score 46 ; DB 2 ; Length 332;				
Matches 8 ; Conservative 2 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;				
RESULT 2				
MLTA_BUCA1 STANDARD ;				
ID MLTA_BUCA1				
AC Q8KS7;				
DT 28-FEB-2003 (Rel. 41, Created)				
DT 05-JUL-2004 (Rel. 44, Last sequence update)				
DE Membrane-bound lyric murine transglycosylase A homolog (EC 3.2.1.-)				
DE (Murine hydrolase A).				
GN Name=mlTA; OrderedLocusNames=BUSq442;				
OS Buchnera aphidicola (subsp. Schizaphis graminum),				
OC Bacteri; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC Enterobacteriaceae; Buchnera.				
NCBI_TaxID=98194; [1]				
RN				

SEQUENCE FROM N.A.; PubMed=12089438; DOI=10.1126/science.1071278;
 RX MEDLINE=22084540; PubMed=12089438; DOI=10.1126/science.1071278;
 RA Tamas I., Klasson L., Canbaek B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:12376-12379 (2002).
 -!- FUNCTION: Murine-degrading enzyme. May play a role in recycling of
 CC muropeptides during cell elongation and/or cell division (By
 CC similarity).
 -!- CATALYTIC ACTIVITY: Cleavage of the beta-1,4-glycosidic bond
 CC between N-acetyl muramic acid and N-acetylgalactosamine residues,
 CC thereby conserving the energy in a newly synthesized 1,6-
 CC anhydrobond in the muramic acid residue.
 -!- SUBCELLULAR LOCATION: In closeley related bacteria this protein is
 CC attached to the outer membrane by a lipid anchor. This is
 CC apparently not the case here.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AP001119; BAB13155.1; -.
 DR InterPro; IPR010611; 3D.
 DR Pfam; PF03562; M1TA_1.
 DR Cell wall; Complete Proteome; Glycosidase; Hydrolase.
 SQ SEQUENCE 359 AA; 41713 MW; 24E12A2778D351AB CRC64;
 Query Match Score 45; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 11; Gaps 0;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPVLDENGIF 10
 Db 298 IPILQNGVF 307
 RESULT 4
 Q8XIG7 PRELIMINARY;
 ID Q8XIG7; PRELIMINARY;
 AC 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Probable inosine-5'-monophosphate dehydrogenase.
 GN Name=gnaB; OrderedLocusNames=CPEZ153;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia;
 OC Clostridiaceae;
 RN [1] NCBI_TaxID=1502;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=13;
 RX MEDLINE=21664373; PubNedd=11792842;
 RA Shimizu T., Ohnai K., Hirakawa H., Oshihara K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003193; BAB1159.1; -.
 DR InterPro; IPR000644; CBS.
 DR Pfam; PF00571; CBS; 2.
 DR SMART; SM00116; CBS; 2.
 DR Complete Proteome;
 SQ SEQUENCE 136 AA; 15608 MW; 36646441544E40AE CRC64;
 Query Match Score 43; DB 2; Length 136;
 Best Local Similarity 60.0%; Pred. No. 9.2%;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IPVLDENGIF 10
 Db 106 VPVVDNGIF 115
 RESULT 5
 Q89YU0 PRELIMINARY;
 ID Q89YU0; PRELIMINARY;
 AC 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 OC Enterobacteriaceae; Buchnera.
 RN [1] NCBI_TaxID=118099;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077; DOI=10.1038/35024074;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.";
 RL Nature 407:81-86 (2000).
 -!- CATALYTIC ACTIVITY: Cleavage of the beta-1,4-glycosidic bond
 CC between N-acetyl muramic acid and N-acetylgalactosamine residues,
 CC thereby conserving the energy in a newly synthesized 1,6-
 CC anhydrobond in the muramic acid residue.
 -!- SUBCELLULAR LOCATION: In closeley related bacteria this protein is

DB	B110955 protein.	Query Match Score 42;	DB 2;	Length 942;
GN	OrderedlocusName=b110955;	Best Local Similarity 54.5%;	Pred No. 1.1e+02;	
OS	Bradyrhizobium japonicum.	Mismatches 4;	Indels 0;	Gaps 0;
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Bradyrhizobiaceae; Bradyrhizobium.			
NCBI_TaxID	375;			
[1]	SEQUENCE FROM N.A.			
SPRINTNAME=USDA110/				
RX	MEDLINEID=22481998; PubMedID=12997275;			
RA	Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watarabe A., Itohara K., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;	Query Match Score 42;	DB 2;	Length 942;
RA	"Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";	Best Local Similarity 54.5%;	Pred No. 1.1e+02;	Mismatches 4;
RT	DNA Res 9:189-197(2002).	Indels 0;	Gaps 0;	
RL	EMBL; A005938; BAC46220.1;			
DR	GO: GO:0004871; P: signal transducer activity; IEA.			
DR	GO: GO:0007165; P: signal transduction; IEA.			
DR	InterPro; IPR001633; EAL.			
DR	InterPro; IPR0000150; GGDEF.			
PFam; PF00990; GGDEF; 1.				
PFam; PF00990; EAL; 1.				
SMART; SMART_0267; DDFP1; 1.				
SMART; SMART_00052; DDFP2; 1.				
SMART; SMART_00091; PAS; 4.				
TIGRFAMs; TIGR00234; GGDEF; 1.				
PROSITE; PS50883; EAL; 1.				
PROSITE; PS50887; GGDEF; 1.				
KW	Complete proteome.			
SEQUENCE 955 AA; 106564 MW; C7C79FAF35CC370A CRC64;				
Query Match Score 42;	DB 2;	Length 942;		
Best Local Similarity 54.5%;	Pred. No. 1.1e+02;	Mismatches 4;	Indels 0;	Gaps 0;
Matches 7;	Conservative 2;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1 IPVLDENGIFAP 12			
Db	754 IPIAEENGLIVP 765			
RESULT 6				
Q6S734	PRELIMINARY;	PRT; 942 AA.		
AC	Q6S734;	Unprecedented genomic diversity of AhR1 and AhR2 genes in Atlantic salmon (Salmo salar L.).";		
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DB	Ary1 hydrocarbon receptor 2b (Fragment).			
GN	Name=AhR2;			
OS	Salmo salar (Atlantic salmon).			
OC	Actinoperygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.			
OX				
[1]	SEQUENCE FROM N.A.			
RA	Hansson M., Wittzell H., Persson K., Von Schantz T.; "Unprecedented genomic diversity of AhR1 and AhR2 genes in Atlantic salmon (Salmo salar L.).";			
RT	Unprecedented genomic diversity of AhR1 and AhR2 genes in Atlantic salmon (Salmo salar L.).";			
RT	Aquac. Toxicol. 0-0 (2004).			
DR	EMBL; AY463927; AAS55735.1; JOINED.			
DR	EMBL; AY463928; AAS55735.1; JOINED.			
DR	GO: GO:0004872; F: receptor activity; IEA.			
DR	InterPro; IPR000014; PAS.			
DR	Receptor; PS50112; PAS; 1.			
KW				
FT	NON_TER 1 102536 MW; 4755COFD7D8AD7EE CRC64;			
SEQUENCE 942 AA; 102536 MW; 4755COFD7D8AD7EE CRC64;				
Qy	1 IPVLDENGIFAP 11			
Db	910 LPVTDNSNGIFS 920			
RESULT 7				
AAS55735	PRELIMINARY;	PRT; 942 AA.		
ID	AAS55735	(TREMBLrel. 27, Created)		
AC	AAS55735	Unprecedented genomic diversity of AhR1 and AhR2 genes in Atlantic salmon (Salmo salar L.).";		
DT	01-JUN-2004 (TREMBLrel. 27, Last sequence update)			
DT	01-JUN-2004 (TREMBLrel. 27, Last annotation update)			
DE	Ary1 hydrocarbon receptor 2b (Fragment).			
GN	Name=AhR2;			
OS	Salmo salar (Atlantic salmon).			
OC	Actinoperygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.			
OX				
[1]	SEQUENCE FROM N.A.			
RA	Hansson M., Wittzell H., Persson K., Von Schantz T., "Two additional AhR2 genes in Atlantic salmon.", Aquat. Toxicol. 0-0 (2004).			
RT				
RL				
RN				
PP				
[2]	SEQUENCE FROM N.A.			
RA	Hansson M.C., Persson K.; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
RL				
RN				
PP				
[3]	SEQUENCE FROM N.A.			
RC	TISSUE=Testis			
RA	Bemanian V., Ladstein S., Goksoyr A., Male R.;			

RL	Submitted (NOV-2003) to the EMBL/GemBank/DBBJ databases.	RP	SEQUENCE FROM N.A.
DR	EMBL; AY19865; CAB46169; -.	RA	Hansson M., Wittzell H., Persson K., Von Schantz T.;
DR	EMBL; AJ008768; CAB75591; -.	RT	"Two additional AhR2 genes in Atlantic salmon.";
DR	GO:0004872; F:receptor activity; IEA.	RL	Aquat. Toxicol. 0:0-0 (2004).
DR	InterPro; IPR00109; HUH_basic.	RN	[2]
DR	InterPro; IPR00104; PAS.	RA	SEQUENCE FROM N.A.
Pfam	Pfam0010; HUH; 1.	RA	Hansson M.C., Persson K.;
DR	Pfam; PF00989; PAS; 1.	DR	Submitted (JAN-2003) to the EMBL/GemBank/DBBJ databases.
SMART	SMART; SM00352; HUH; 1.	EMBL; AY219865; AAP46169; -.	
DR	PROSITE; PS00091; PAS; 2.	KW	Receptor.
DR	PROSITE; PS50888; HUH; 1.	SEQUENCE	1058 AA; 115396 MW; AFD7FE2D1BA91061 CRC64;
DR	PROSITE; PS50112; PAS; 1.	Query Match	66.7%; Score 42; DB 2; Length 1058;
Receptor.	SEQUENCE 1058 AA; 115396 MW; AFD7FE2D1BA91061 CRC64;	Best Local Similarity	54.5%; Pred. No. 1.2e+02;
kw	Qy 1 IPVLIDENG1F1A 11	Matches	5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
SQ	Db 1026 LPVIDSNGIFS 1036	Db	1026 LPVIDSNGIFS 1036
<hr/>			
RESULT 9		RESULT 11	
CAF75591	PRELIMINARY;	Q8CM69	PRELIMINARY;
ID	CAB46169;	ID	PRT; 1576 AA.
AC	CAF75591;	AC	Q8CM69;
DT	14-APR-2004 (TREMBLrel. 27, Created)	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	14-APR-2004 (TREMBLrel. 27, Last sequence update)	DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DT	14-APR-2004 (TREMBLrel. 27, Last annotation update)	DB	Hypothetical protein gbs0386 (Hypothetical protein gbs0716)
DB	Aryl hydrocarbon receptor 2 beta.	DE	(Hypothetical protein gbs0933).
GN		GN	Orderredocnames-gbs0386, gbs0716, gbs0933;
OS	Salmo salar (Atlantic salmon).	OS	Streptococcus agalactiae NEM316.
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	OC	Streptococcus agalactiae serogroup III.
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.	RN	[1]
NCBI_TaxID=8030;	RN_OX	RN_OX	NCB_1_TaxID=211110;
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE/Testis;	RC	STRAIN=NEM316 / Serotype III;
RA	Manelian V., Ladstein S., Goksoyr A., Male R.;	RA	MEDLINE=22242508; Published=12354221;
RT	"Molecular cloning and tissue specific expression of two novel variants of the Aryl Hydrocarbon Receptor (AHR) from Atlantic salmon (Salmo salar)."	RA	Glaser P., Rusnick C., Buchrieser C., Chevalier P., Frangeul L., Maedek T., Zouine M., Couve E., Laloui L., Poyart C., trieu-Cuot P., Kunz F.;
RT	Submitted (NOV-2003) to the EMBL/GemBank/DBBJ databases.	RT	"Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease";
RL	DR; EMBL; AJ608768; CAB75591; -.	RL	Mol. Microbiol. 45:149-1513 (2002).
DR	Receptor.	DR	EMBL; AL766845; CAD4630; -;
DR	SEQUENCE 1058 AA; 115396 MW; AFD7FE2D1BA91061 CRC64;	DR	EMBL; AL766846; CAD43360; -;
kw	Qy 1 IPVLIDENG1F1A 11	DR	EMBL; AL766848; CAD46655; -;
SQ	Db 1026 LPVIDSNGIFS 1036	DR	Sagaliste; gbs0386; -;
<hr/>			
RESULT 10		RESULT 12	
AAP46169	PRELIMINARY;	Q7CS40	PRELIMINARY;
ID	AAP46169;	ID	PRT; 180 AA.
AC	AAP46169;	AC	Q7CS40;
DT	01-JUN-2004 (TREMBLrel. 27, Created)	DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	01-JUN-2004 (TREMBLrel. 27, Last sequence update)	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DB	Aryl hydrocarbon receptor 2 beta.	DB	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
OS	Salmo salar (Atlantic salmon).	OS	Actinopterygii; Chordata; Craniata; Vertebrata; Euteleostei;
OC	Bukaryota; Metazoa; Neopterygii; Teleostei; Euteleostei;	OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.	RN	[1]
NCBI_TaxID=8030;	RN	RESULT 10	
RR	SEQUENCE FROM N.A.	Qy 1 IPVLIDENG1F1A 11	Query Match
RR	RT	Best Local Similarity	66.7%; Score 42; DB 2; Length 1576;
RR	RT	Matches	8; Conservative 100%; Mismatches 0; Indels 0; Gaps 0;
RR	RR	Db	1315 IPVLIDENG1F1A 11

OrderedLocusNames=AGR L_3019;			
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970);			
OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;			
CC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium;			
OX NCBI_TaxID=176299;			
RN [1]	SEQUENCE FROM N.A.		
RN STRAIN=Cereon;			
RX MEDLINE=21608551; PubMed=11743194;			
RX Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Halling C., Mullin L.,			
RX Quroli K., Gordon B.S., Cao Y., Astenazi M., Tarchouk O., Epp A., Liu F.,			
RX Houriem K., Gordon J., Vaudin M., Tarchouk O., Epp A., Scott C., Lappas C., Markelz B.,			
RX Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Strub G.,			
RX Flanagan C., Crowley C., Gurson J., Lomo C., Sear C., Strub G.,			
RX Cielo C., Slater S.;			
RX "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";			
RX RLU Science 294:2323-2328 (2001).			
RX DR EMBL; AE008353; AAK0091.1; -.			
RX DR InterPro; IPR000020; DUF6.			
RX PFam; PF00892; DUF6; 1.			
RX SQ SEQUENCE 180 AA; 19735 MW; 71D0FF440AE034FF0 CRC64;			
Query Match 65.1%; Score 41; DB 2; Length 180;			
Best Local Similarity 50.0%; Pred. No. 29;			
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;			
Qy 1 IPVLDENGFLP 12			
Db 7 VPALNENGFYRP 18			
RESULT 13			
Q6XIF9 PRELIMINARY;	PRT;	209 AA.	
ID Q6XIF9			
AC Q6XIF9;			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DR Similar to Drosophila melanogaster CG17524 (Fragment).			
OS Drosophila yakuba (Fruit fly).			
OC Eukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC Drosophilidae; Drosophila.			
OX NCBI_TaxID=7245;			
RN SEQUENCE FROM N.A.			
RN STRAIN=Cereon;			
RX MEDLINE=21608551; PubMed=11743194;			
RX Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Halling C., Mullin L.,			
RX Quroli K., Gordon B.S., Cao Y., Astenazi M., Tarchouk O., Epp A., Scott C., Lappas C., Markelz B.,			
RX Houriem K., Gordon J., Vaudin M., Tarchouk O., Epp A., Scott C., Lappas C., Strub G.,			
RX Flanagan C., Crowley C., Gurson J., Lomo C., Sear C., Strub G.,			
RX Cielo C., Slater S.;			
RX "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";			
RX RLU Science 294:2323-2328 (2001).			
RX DR EMBL; AE008353; AAK0091.1; -.			
RX DR InterPro; IPR000020; DUF6.			
RX PFam; PF00892; DUF6; 1.			
RX SQ SEQUENCE 180 AA; 19735 MW; 71D0FF440AE034FF0 CRC64;			
Query Match 65.1%; Score 41; DB 2; Length 180;			
Best Local Similarity 50.0%; Pred. No. 34;			
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
Qy 1 IPVLDENGFLP 10			
Db 55 VPVLDNGFY 64			
RESULT 14			
Q6XIF9 PRELIMINARY;	PRT;	209 AA.	
ID Q6XIF9			
AC Q6XIF9;			
DT 03-JAN-1998 (TREMBLrel. 05, Created)			
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DR Name=Orf12;			
OS Bacillus megaterium.			
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
RN NCBI_TaxID=1404;			
RN SEQUENCE FROM N.A.			
RN Vazquez G.J.; Pettinari M.J.; Mendez B.M.; Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.			
RN [1]			
RN SEQUENCE FROM N.A.			
RX MEDLINE=22887302; PubMed=11525923;			
RX Domazet-Loso T.; Tautz D.			
RX "An evolutionary analysis of orphan genes in Drosophila.";			
RX Genome Res. 13:2213-2219 (2003).			
RX "- SIMILARITY: Belongs to the GST superfamily.			
DR EMBL; AY231871; AR09844.1; -.			
DR InterPro; IPR004046; GST_Cterm.			
DR InterPro; IPR010387; GST_C-like.			
DR InterPro; IPR004045; GST_N-term.			
DR PFam; PF00043; GST_C_1.			
DR PFam; PF002798; GST_N_1.			
FT NON_TER 1 209 AA; 23559 MW; 5D6A8D4F6F13DC5C CRC64;			
SQ SEQUENCE 209 AA; 23559 MW; 5D6A8D4F6F13DC5C CRC64;			
Query Match 65.1%; Score 41; DB 2; Length 209;			
Best Local Similarity 60.0%; Pred. No. 34;			
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
Qy 1 IPVLDENGFLP 10			
Db 55 VPVLDNGFY 64			
RESULT 15			
Q31394 PRELIMINARY;	PRT;	245 AA.	
ID Q31394;			
AC Q31394;			
DT 031394; (TREMBLrel. 05, Created)			
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DR Sensory transduction histidine kinase.			
GN Name=Orf12;			
OS Bacillus megaterium.			
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
RN NCBI_TaxID=1404;			
RN SEQUENCE FROM N.A.			
RN Vazquez G.J.; Pettinari M.J.; Mendez B.M.; Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RN SEQUENCE FROM N.A.			
RA Mendez B.S.; Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.			
RL DR EMBL; Y14588; CAA4928.1; -.			
DR GO; GO:0016301; F-kinase activity; IEA.			
DR GO; GO:0004871; F-signal transduction activity; IEA.			
DR GO; GO:0007165; P-signal transduction; IEA.			
DR InterPro; IPR00014; PSS.			
DR Pfam; PF00989; PAS; 1.			
DR SMART; SM00091; PAS; 1.			
DR TIGRFAMS; TIGR00229; sensory_box_1.			
DR PROSITE; PS55112; PAS; 1.			
KW Kinase.			
SQ SEQUENCE 245 AA; 27391 MW; 6B6E2A39BB25E7C1 CRC64;			
Query Match 65.1%; Score 41; DB 2; Length 245;			
Best Local Similarity 87.5%; Pred. No. 41;			
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 IPVLDENGFLP 8			
Db 199 : :			
Qy 1 IPVLDENGFLP 206;			
Db 199 IPVLDNGFY 206			

Q6FMK9	PRELIMINARY;	PRT;	320 AA.	RL	Nat. Biotechnol. 22:554-559 (2004) .
ID Q6FMK9				DR EMBL; AE017318; AAS97062.1;	.
AC				DR TIGR; DV02590; -	.
DT 05-JUL-2004	(TREMBLrel. 27, Created)			DR InterPro; IPR007380; DUF438.	
DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)			DR InterPro; IPR000577; FGGY_Kin.	
DT 05-JUL-2004	(TREMBLrel. 27, Last annotation update)			DR Pfam; PF04282; DUF338; 1.	
GN ORFNAMES=sp P12904 Saccharomyces cerevisiae YGL115w SNF4.				DR PROSITE; PS00045; FGGY_MINASES_2; UNKNOWN_1	
OS Candida glabrata (Yeast) (Torulopsis glabrata).				KW Complete proteome.	
OC Saccharomyces; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				SEQUENCE 521 AA; 57195 MW; 837255C37877532C CRC64;	
OX NCBI_TAXID=5478;					
RN [1]	SEQUENCE FROM N.A.				
RC STRAIN=CBS138;					
RG					
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Talla E., Lafontaine I., de Montigny J., March C., Neuveglise C., Bleykasten C., Barde V., Goffard L., Aigle M., Anthouard V., Babour A., Barde V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confiolioli F., de Darvvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hemeunier C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Kobzuk R., Lenaire M., Lesur I., Ma L., Muller H., Niclou M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennne D., Tekaya F., Wesolowski-Louvel M., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Rukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souillet J.L., RT "Genome evolution in yeasts." Nature 430:35-44 (2004).					
RL					
DR EMBL; CR380957; CAG61496.1; -.					
DR InterPro; IPR006644; CBS.					
DR SMART; SM00116; CBS; 4.					
SQ SEQUENCE 320 AA; 36478 MW; EB736BAE06FF5737 CRC64;					
Query Match 65.1%; Score 41; DB 2; Length 320;					
Best Local Similarity 66.7%; Pred. No. 54;					
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;					
QY 1 IPVLDENG 9					
Db 223 VPILDENG 231					
RESULT 17					
ID Q728L3	PRELIMINARY;	PRT;	521 AA.	Query Match 65.1%; Score 41; DB 2; Length 521;	
AC				Best Local Similarity 63.6%; Pred. No. 90;	
DT 05-JUL-2004	(TREMBLrel. 27, Created)			Matches 3; Mismatches 1; Indels 0; Gaps 0;	
DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)				
DE Sensory box protein.					
GN OrderedLocusNames=DVO2590;					
OS Debifloribacter vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).					
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales; Desulfobacteriaceae; Desulfobacterio.					
OX NCBI_TAXID=882;					
RN [1]	SEQUENCE FROM N.A.				
RP					
RX PubMed=15077118; DOI=10.1038/nbt959;					
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Zafar N., Haft D.H., Radue D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Peterson J.D., Davidsen T.M., Zhou L., Voordouw G., Fraser C.M., Feldblyum T.V., Wall J.D., "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfobacter vulgaris Hildenborough.", Nat. Biotechnol. 22:554-559 (2004). DR EMBL; AE017318; AAS97062.1; -.					
DR TIGR; DV02590; -					
SQ SEQUENCE 521 AA; 57195 MW; 837255C37877532C CRC64;					
RESULT 18					
ID AAS97062	PRELIMINARY;	PRT;	521 AA.	Query Match 65.1%; Score 41; DB 2; Length 521;	
AC AAS97062;				Best Local Similarity 63.6%; Pred. No. 90;	
DT 26-APR-2004	(TREMBLrel. 27, Created)			Matches 3; Mismatches 1; Indels 0; Gaps 0;	
DT 26-APR-2004	(TREMBLrel. 27, Last sequence update)				
RA Sensory box protein.					
GN DV0590.					
OS Debifloribacter vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).					
OS Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales; Desulfobacteriaceae; Desulfobacterio.					
OX NCBI_TAXID=882;					
RN [1]	SEQUENCE FROM N.A.				
RP					
RX PubMed=15077118; DOI=10.1038/nbt959;					
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Zafar N., Haft D.H., Radue D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Peterson J.D., Davidsen T.M., Zhou L., Voordouw G., Fraser C.M., Feldblyum T.V., Wall J.D., "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfobacter vulgaris Hildenborough.", Nat. Biotechnol. 22:554-559 (2004). DR EMBL; AE017318; AAS97062.1; -.					
DR TIGR; DV02590; -					
SQ SEQUENCE 521 AA; 57195 MW; 837255C37877532C CRC64;					
RESULT 19					
ID Q7VRX7	PRELIMINARY;	PRT;	696 AA.	Query Match 65.1%; Score 41; DB 2; Length 521;	
AC Q7VRX7;				Best Local Similarity 63.6%; Pred. No. 90;	
DT 01-OCT-2003	(TREMBLrel. 25, Created)			Matches 3; Mismatches 1; Indels 0; Gaps 0;	
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)				
RA Sensory box protein.					
GN Name1=iga; Synonym=dhaI.					
RA Bordetella pertussis.					
RA Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetellae.					
OC NCBI_TAXID=520;					
RN [1]	SEQUENCE FROM N.A.				
RP					
RX PubMed=15077118; DOI=10.1038/nbt959;					
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Zafar N., Haft D.H., Radue D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Peterson J.D., Davidsen T.M., Zhou L., Voordouw G., Fraser C.M., Feldblyum T.V., Wall J.D., "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfobacter vulgaris Hildenborough.", Nat. Biotechnol. 22:554-559 (2004). DR EMBL; AE017318; AAS97062.1; -.					
DR TIGR; DV02590; -					
SQ SEQUENCE 521 AA; 57195 MW; 837255C37877532C CRC64;					

RP	SEQUENCE FROM N.A.	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
RC	STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;	
RX	MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;	
RA	Harris D.E., Sebaldin M., Preston A., Murphy L.D., Thomson N.R., Parkhill J., Sebaldin M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achim M., Atkin R., Baker S., Basham D., Bason N., Chervach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabinowitzsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skellon J., Squares R., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; RT "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica.";	
RA	Nat. Genet. 35:32-40 (2003).	
CC	-!- FUNCTION: This protein catalyzes the formation of phosphodiester linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-stranded DNA using NAD as a coenzyme and as the energy source for the reaction. It is essential for DNA replication and repair of damaged DNA. (By similarity).	
CC	-!- CATALYTIC ACTIVITY: NAD(+) + {deoxyribonucleotide}(N) + {deoxyribonucleotide}(M) = AMP + nicotinamide nucleotide + (deoxyribonucleotide)(N-M). Belongs to the NAD-dependent DNA ligase family.	
CC	-!- SIMILARITY: Belongs to the NAD-dependent DNA ligase family.	
DR	EMBL: B6640421; IPRO01357; BRCT.	
DR	GO:0005622; Cintracellular; IEA.	
DR	GO:0003677; P:DNA binding; IEA.	
DR	GO:0003911; P:DNA ligase (NAD+); activity; IEA.	
DR	GO:00016874; P:ligase activity; IEA.	
DR	GO:0006281; P:DNA repair; IEA.	
DR	IPRO00421; CRB3819_1.	
DR	GO:0005622; Cintracellular; IEA.	
DR	GO:0003677; P:DNA binding; IEA.	
DR	GO:0003911; P:DNA ligase (NAD+); activity; IEA.	
DR	GO:00016874; P:ligase activity; IEA.	
DR	GO:0006281; P:DNA repair; IEA.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	InterPro; IPRO01357; BRCT.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO003583; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR	IPRO004149; Znf_DNAligase_OB.	
DR	IPRO001679; DNAligase.	
DR	IPRO004150; P:DNA ligase_OB.	
DR	IPRO00445; HHH.	
DR	IPRO006260; P:DNA replication; IEA.	
DR	IPRO004149; Znf_DNAligase_C4.	
PFAM	PF00533; BRCT [*] ; 1.	
DR</td		

01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE DNA ligase (EC 6.5.1.2).
 GN Name=ligA; Synonyms=dnaL, lig, lop, lodeC; OrderedLocusNames=BB3804;
 OS Bordetellina bronchiseptica (Alcaligenes bronchiSepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 Alcaligenaceae; Bordetellales;
 NCBI_TaxID=518;

[1] N
 RP SEQUENCE FROM N.A.
 RX STRAIN=B850 / ATCC BAA-588;
 RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
 RA Parkhill J., Sebastian M., Preston A., Murphy L.D., Thomson N.R.,
 Cerdeno-Taraga A.-M., Churcher C.M., Bentley S.D., Mungall K.L.,
 Achtmann M., Atkin R., Baker S., Basham D., Bascon N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
 Sharp S., Simmonds M., Skelton J., Squares R., Saunders D., Seeger K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J./
 RR Comparative analysis of the genome sequences of *Bordetella pertussis*,
Bordetella parapertussis and *Bordetella bronchiseptica*.";
 RL Nat. Genet. 35:32-40 (2003).

[CC] FUNCTION: This protein catalyzes the formation of phosphodiester
 linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-
 stranded DNA using NAD as a coenzyme and as the energy source for
 the reaction. It is essential for DNA replication and repair of
 damaged DNA (By similarity).
 [-] CATALYTIC ACTIVITY: NAD(+) + {deoxyribonucleotide}{N} +
 {deoxyribonucleotide}{(N+M)} = AMP + nicotinamide nucleotide +
 {deoxyribonucleotide}{(N+M)}.
 [-] SIMILARITY: Belongs to the NAD-dependent DNA ligase family.

DR EMBL; BX640448; EAB35778.1; -.
 DR GO; GO:0005222; C: intracellular; IEA.
 DR GO; GO:0003677; P: DNA binding; IEA.
 DR GO; GO:0003911; P: DNA ligase (NAD⁺) activity; IEA.
 DR GO; GO:0016874; P: ligase activity; IEA.
 DR GO; GO:000281; P: DNA repair; IEA.
 DR GO; GO:0006260; P: DNA replication; IEA.
 DR InterPro; IPR001357; BRCT.
 DR InterPro; IPR001679; DNA_ligase.
 DR InterPro; IPR004150; DNA_ligase_OB.
 DR InterPro; IPR000445; Hhh.
 DR InterPro; IPR003583; Hhh.1.
 DR InterPro; IPR004149; Znf_DNAligase_C4.
 DR Pfam; PF00533; BRCT; 1.
 DR SMART; SM001653; DNA_ligase_aden; 1.
 DR Pfam; PF03120; DNA_ligase_OB; 1.
 DR Pfam; PF0119; DNA_ligase_ZBD; 1.
 DR ProDom; P0003944; DNAligase; 1.
 DR SMART; SM00292; BRCT; 1.
 DR SMART; SM00278; HhhH; 4.
 DR TIGRFAM; TIGR00575; dnaj; 1.
 DR PROSITE; PS001055; DNA_LIGASE_N1; 1.
 DR PROSITE; PS01056; DNA_LIGASE_N2; 1.
 KW Complete proteome; DNA repair; DNA replication; Ligase; NAD.
 SQ SEQUENCE 696 AA; 75555 MW; CBB417/DB183/TEAS CRC64;

Query Match 65.1%; Score 41; DB 2; Length 696;
 Best Local Similarity 72.7%; Pred. No. 1.2e+02; Indels 0; Gaps 0;

Qy 1 IPVLDENGFLFAP 12
 :|||||:|||:
 Db 682 VPVLDEHGQMTP 297

RESULT 23
 ID Q83WMB8 PRELIMINARY;
 AC Q83WMB8 PRELIMINARY;
 ID Q83WBB8 PRELIMINARY;
 AC Q83WBB8 PRELIMINARY;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE DNA gyrase subunit B.
 GN Name=parYR;
 OS Streptomyces rishiriensis.
 OC Bacteria; Actinobacteria; Actinomycetales; Streptomyces.
 OC Streptomycineae; Streptomyctaceae; Streptomyces.

OX NCBI_TaxID=68264;	RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.;
SEQUENCE FROM N.A.	
RN [1]	RA "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)"
RC STRAIN=DM 40489;	RT RT
RX MEDLINE=22491493; PubMed=12604514;	RL Nature 417:141-147(2002).
RA Schmitz B., Muehlenweg A., Li S.-M., Heide L.;	CC FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).
RT Resistance genes of aminocoumarin producers: two type II topoisomerase genes confer resistance against coumetmycin A1 and clorobiocin."	CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
RL Antimicrob Agents Chemother. 47:169-187(2003).	CC -I- SIMILARITY: Belongs to the type II topoisomerase family.
CC -I- FUNCTION: DNA gyrase negatively supercoils closed circular double-stranded DNA in an ATP-dependent manner and also catalyzes the interconversion of other topological isomers of double-stranded DNA rings, including catenanes and knotted rings (By similarity).	CC EMBL: AL939125; CRA18520.1; -.
CC -I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.	DR PIR: T35196; T35196.
CC -I- SIMILARITY: Belongs to the type II topoisomerase family.	DR HSSP: P06982; IAJG.
DR EMBL: AP205853; AAQ47226.1; -.	DR GO: GO:0005524; F:ATP binding; IEA.
DR HSSP: P06982; 1KZN;	DR GO: GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.	DR GO: GO:0003677; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006304; P:DNA binding; IEA.	DR GO: GO:0006304; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.	DR InterPro: IPR03524; ATPbind_ARPase.
DR GO; GO:0006304; P:DNA modification; IEA.	DR InterPro: IPR002288; DNA_gyraseB_C.
DR GO; GO:0006265; P:DNA topological change; IEA.	DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR003594; ATPbind_ARPase.	DR InterPro: IPR001241; DNA_topoisom.
DR InterPro: IPR002288; DNA_gyraseB_C.	DR InterPro: IPR006171; Toprim dom.
DR InterPro: IPR011558; DNA_gyrase_B.	DR PFam: PF00204; DNA_gyraseB_1.
DR InterPro: IPR001241; DNA_topoisom.	DR PFam: PF00986; DNA_gyraseB_C_1.
DR InterPro: IPR006171; Toprim_dom.	DR PFam: PF02518; HATPase_c_1.
DR PFam: PF00204; DNA_gyraseB_1.	DR PFam: PF01751; Toprim_1.
DR PFam: PF00986; DNA_gyraseB_C_1.	DR PRINTS: PR00418; TP12FAMILY.
DR PFam: PF02518; HATPase_c_1.	DR PRODOM: PD149633; DNA_gyrase_B_1.
DR PFam: PF01751; Toprim_1.	DR SMART: SM00387; HATPase_C_1.
DR PROSITE: PS00418; TP12FAMILY.	DR SMART; SM00433; TOP2C_1.
DR SMART; SM0149533; DNA_gyrase_B_1.	DR PROSITE; PS000177; TOPOISOMERASE_III; UNKNOWN_1.
DR SMART; SM00387; HATPase_c_1.	DR PROSITE; PS000177; TOPOISOMERASE_III; UNKNOWN_1.
DR PROSITE: PS00177; TOP2C_1.	KW ATP-binding; Complete proteome; Isomerase; Topoisomerase.
DR ATP-binding; Isomerase; Topoisomerase.	KW PROSITE; PS000177; TOP2C_1.
SEQUENCE 702 AA; 7684 MW; DB1B6665B075D18 CRC64;	KW SEQUENCE -707 AA; 77269 MW; 1A5427BB8EFB661 CRC64;
Query Match 65.1%; Score 41; DB 2; Length 707;	Query Match 65.1%; Score 41; DB 2; Length 707;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;	Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0;	Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 IPVLDENGIFAP 12	QY 1 IPVLDENGIFAP 12
Db 285 VPVLDDEHGQMTP 296	Db 290 VPVLDDEHGQMTP 301
RESULT 25	RESULT 25
Q6CPB9	Q6CPB9
ID Q6CPB9; PRELIMINARY;	ID Q6CPB9; PRELIMINARY;
AC AC	AC Q6CPB9; PRELIMINARY;
DT DT	DT DT
01-OCT-2004 (TREMBrel. 28, Created)	01-OCT-2004 (TREMBrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBrel. 28, Last annotation update)	DT 01-OCT-2004 (TREMBrel. 28, Last annotation update)
DT Strain NRRL Y-1140 chromosome B of strain NRR Y-1140 of Kluyveromyces lactis.	DB Strain NRRL Y-1140 chromosome B of strain NRR Y-1140 of Kluyveromyces lactis.
GN ORFnames-KLIA0E06028g;	GN ORFnames-KLIA0E06028g;
OS Kluyveromyces lactis (Yeast);	OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetae; Kluyveromyces.
OC NCBITaxID=28985;	OC NCBITaxID=28985;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC GENOMEVERSION;	RC GENOMEVERSION;
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marc C., Neuveglise C., Talla E., Goiffard N., Frangoul L., Aigle M., Anthouard V., Babur A., Barbé V., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykauskas C., Boistrame A., Boyer J., Cattolico L., Conflancieri M., Darvarov A., Desnoes L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,	

DR	HSSP; Q9CNE9; 1JLV.	RP	SEQUENCE FROM N.A.
IntAct	Q9V866; -	RC	STRAIN=ZAN/U;
DR	FlYBase; FBgn0034135; GstB1.	RX	PubMed=12914673;
DR	GO; GO:0016740; GST transferase activity; IEA.	RA	Ding Y., Ortelli F., Rossiter L.C., Hemingway J., Ranson H.; RT "The Anopheles gambiae glutathione transferase supergene family: annotation, phylogeny and expression profiles." ;
DR	InterPro; IPR004066; GST_Cterm.	RT	RT annotation, phylogeny and expression profiles. ;
InterPro; IPR010987; GST_C_like.		RL	BMC Genomics 4:35-35 (2003).
InterPro; IPR004055; GST_Nterm.		RN	[12]
DR	Pfam; PF000443; GST_C; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF02798; GST_N; 1.	RC	Ranson H.A., Ortelli F.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
KW	Transferase.	RA	-!- SIMILARITY: Belongs to the GST superfamily.
SEQUENCE 224 AA;	24959 MW; 148C2F159DBBC806 CRC64;	RL	EMBL: AF515521; AAC61888.1; -.
Best Local Similarity 60.0%; Pred. No. 57;	Score 40; DB 2; Length 224;	CC	DR HSSP; Q9CNE9; 1JLV.
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;		DR GO; GO:0016740; F; transferase activity; IEA.	
Qy 1 IPVLDENGIF 10		DR InterPro; IPR004046; GST_Cterm.	
Db 57 VPMLDDNGTF 66		DR InterPro; IPR010987; GST_C_like.	
		DR Pfam; PF000443; GST_C; 1.	
		DR Pfam; PF02798; GST_N; 1.	
RESULT 34		KW Transferase.	
Q7PSW6	PRELIMINARY;	SQ SEQUENCE 233 AA;	26064 MW; AB3222CAB0CC0FA3 CRC64;
ID Q7PSW6	PRT; 233 AA.	Query Match	63.5%; Score 40; DB 2; Length 233;
AC		Best Local Similarity 70.0%; Pred. No. 59;	Mismatches 2; Gaps 0;
DT 01-MAR-2004 (TREMBLrel. 26, Created)		DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)		DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		DE Hypothetical protein OSJNBA0078N1132.	
ENSANGP0000018720		GN Name=OSJNBA0078N1132;	
GN Name=ENSANGG0000016231;		OS Oryza sativa (Japonica cultivar-group).	
Anopheles gambiae str. PEST.		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.		OC Ehrhartoidea; Oryzeae; Oryza.	
NCBI TaxID=180454;		OX NCBI_TaxID=39947;	
[1]		RN [1]	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	ANOPHELES Genome Sequencing Consortium;	Q6TWW2	PRELIMINARY;
RA	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.	AC	PRT; 236 AA.
RL	-!- SIMILARITY: Belongs to the GST superfamily.	DT	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an	DT	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
CC	EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is	DR	Submitted (APR-2004) (TREMBLrel. 27, Last sequence update)
CC	preliminary data.	DE	Submitted (APR-2004) (TREMBLrel. 27, Last annotation update)
DR	EMBL: AAB01008811; EAA04937.2; -.	GN	DE Hypothetical protein OSJNBA0078N1132.
DR	InterPro; IPR004046; GST_Cterm.	OS	GN Name=OSJNBA0078N1132;
DR	Pfam; PF000443; GST_C; 1.	OC	OS Oryza sativa (Japonica cultivar-group).
DR	Pfam; PF02798; GST_N; 1.	OC	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SEQUENCE 233 AA;	-26064 MW; AB3222CAB0CC0FA3 CRC64;	OC	OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Qy 1 IPVLDENGIF 10		OC	OC Ehrhartoidea; Oryzeae; Oryza.
Db 52 IPVLDDGGFF 61		OX	OX NCBI_TaxID=39947;
		RN	RN [1]
RESULT 35		RP	SEQUENCE FROM N.A.
QBMTQ6	PRELIMINARY;	Q6TWW2	PRELIMINARY;
ID QBMTQ6	PRT; 233 AA.	AC	PRT; 236 AA.
AC QBMTQ6		DT	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DT 01-OCT-2002 (TREMBLrel. 22, Created)		DR	Submitted (APR-2004) (TREMBLrel. 27, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)		DE	Submitted (APR-2004) (TREMBLrel. 27, Last annotation update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)		GN	DE Hypothetical protein OSJNBA0078N1132.
Name=GST1;		OS Anopheles gambiae (African malaria mosquito).	
Anopheles gambiae (African malaria mosquito).		OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
Eukaryota; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.		OC NCB-TaxID=7165;	
NCB-TaxID=7165;		OX NCBI_TaxID=7165;	
[1]			
RESULT 36		RP	SEQUENCE FROM N.A.
Q6TWW2	PRELIMINARY;	Q6TWW2	PRELIMINARY;
ID Q6TWW2	PRT; 233 AA.	AC	PRT; 236 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)		DT	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)		DR	Submitted (APR-2004) (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein OSJNBA0078N1132.		DE	Submitted (APR-2004) (TREMBLrel. 27, Last annotation update)
GN Name=OSJNBA0078N1132;		GN	GN Name=OSJNBA0078N1132;
OS Oryza sativa (Japonica cultivar-group).		OS	OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		OC	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		OC	OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidea; Oryzeae; Oryza.		OC	OC Ehrhartoidea; Oryzeae; Oryza.
RN [1]		RN	RN [1]
RESULT 37		RP	SEQUENCE FROM N.A.
BAD16458	PRELIMINARY;	Q6TWW2	PRELIMINARY;
ID BAD16458	PRT; 233 AA.	AC	PRT; 236 AA.
AC BAD16458		DT	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DT 23-APR-2004 (TREMBLrel. 27, Last sequence update)		DR	Submitted (APR-2004) (TREMBLrel. 27, Last sequence update)
DT 23-APR-2004 (TREMBLrel. 27, Last annotation update)		DE	Submitted (APR-2004) (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein OSJNBA0078N1132.		GN	GN Name=OSJNBA0078N1132;
OS Anopheles gambiae (African malaria mosquito).		OS	OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		OC	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC NCB-TaxID=7165;		OC	OC NCB-TaxID=7165;
[1]			

OS	Oryza sativa (japonica cultivar-group)	DT	01-MAR-2004 (TREMBLrel. 26, Created)	
OC	Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	
OC	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
OC	Ehrhartoidae; Oryzeae; Oryza; Oryza sativa.	DB	Transcriptional regulator.	
NCBI_TaxID=39947;	[1]	GN	Name=OV2633;	
RN	OS	Vibrio vulnificus (strain YJ016).		
RP	Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;	OC	Vibrionaceae; Vibrio.	
STRAIN=cv.	Nipponbare;	OC		
RC		OX		
RA	Sasaki T., Matsumoto T., Katayose Y.; DNA, chromosome 2, BAC	RN		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC	SEQUENCE FROM N.A.		
RT	clone OSUrn0078N11;"	CC		
RL	Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.	
DR	EMBL: AP005848; BADI6458.1; -.	RX	Published=165695;	
KW	Hypothetical protein.	RA	Chen C.-Y., Wu K.-M., Chang Y.-C., Tsai H.-C., Su T.-L.,	
SEQUENCE	236 AA; 24733 MW; 44E1653230F7395 CRC64;	RA	Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C.,	
SQ		RA	Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.,	
Query Match	Best Local Similarity 63.5%; Score 40; DB 2; Length 236;	RT	"Comparative genome analysis of <i>Vibrio vulnificus</i> , a marine	
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	RT	pathogen.",		
Qy	2 FVLDENGIFAP 12	RT	RT	
Db	3 PFLDEQGLAAP 13	RL	Genome Res. 13: 2577-2587 (2003).	
RESULT 38	Q841U3	PRELIMINARY;	RL	-1 SIMILARITY: Contains 1 HTH laci-type DNA-binding domain.
ID	Q841U3	PRTR;	CC	EMBL; AP005340; BAC95398.1.
AC	Q841U3;	PRTR;	DR	GO; GO:0005622; C: intracellular; IBA.
DT	01-JUN-2003	PRTR;	DR	GO; GO:0003700; F: transcription factor activity; IEA.
DT	01-JUN-2003	PROSITE;	DR	GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DT	01-MAR-2004	PROSITE;	DR	InterPro; IPR000843; HTH Laci.
DE	Laci-1.	PFam;	DR	InterPro; IPR001761; PeriplaBP/Laci.
OS	Vibrio vulnificus.	PRINTS;	DR	Pfam; PRO3356; Laci; 1.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	PRINTS;	DR	PRINTS; PR00336; HTHLACT1.
Vibrionaceae; Vibrio.		PROSITE;	DR	PROSITE; PS00356; HTH_LACI_1; 1.
NCBI_TaxID=672;	[1]	PROSITE;	DR	PROSITE; PS50932; HTH_LACI_2; 1.
RN	SEQUENCE FROM N.A.	DNA-binding;	KW	DNA-binding; Transcription regulation.
RP	STRAIN=ATCC 293307;	SEQUENCE	SQ	SEQUENCE 333 AA; 36097 MW; 8BD8D51793677FFB CRC64;
RC		Query Match	63.5%;	Score 40; DB 2; Length 333;
RA	Baeck C.H., Kim I.H., Kim K.S.;	Best Local Similarity	66.7%;	Best Local Similarity 66.7%; Pred. No. 87;
RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	Matches	8;	Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC	-1 SIMILARITY: Contains 1 HTH laci-type DNA-binding domain.	RESULT 40		
CC		Q8DBN6	PRELIMINARY;	
DR	HSSP; P03023; 1LCC	AC	Q8DBN6;	
DR	GO; GO:0005622; C: intracellular; IBA.	DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DR	GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DR	InterPro; IPR000843; HTH Laci.	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DR	InterPro; IPR010982; Lambda like DNA.	DE	Transcriptional regulator.	
DR	PFam; PF0001761; PeriplaBP/Laci1.	GN	OrderedocusnamesAV1175;	
DR	PFam; PF00356; Laci; 1.	OS	Vibrio vulnificus.	
DR	PRINTS; PR00036; Peripla_BP_1; 1.	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	
DR	SMART; SM00334; HTHLACT1; 1.	OC	Vibrionaceae; Vibrio.	
DR	PROSITE;	RA	NCBI_TaxID=672;	
DR	PS00356; HTH_LACI_1; 1.	RN	SEQUENCE FROM N.A.	
DR	PROSITE; PS59932; HTH_LACI_2; 1.	RC	STRAIN=CMCP6;	
KW	DNA-binding; Transcription regulation.	RA	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	
SEQUENCE	333 AA; 36097 MW; BF1E151EB5A77FFF CRC64;	RA	Choi H.E.,	
SQ		RT	"Complete genome sequence of <i>Vibrio vulnificus</i> CMCP6."	
Query Match	63.5%;	RT	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.	
Best Local Similarity	66.7%;	RT	-1 SIMILARITY: Contains 1 HTH laci-type DNA-binding domain.	
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	1 IPVLDENGIFAP 12	CC	DR	
Qy	1 IPVLDENGIFAP 12	DR	AB016002; AA010186.1; -	
Db	253 LSVDENGILKVP 264	DR	HSSP; P03023; 1LCC.	
RESULT 39		DR	GO; GO:0005622; C: intracellular; IBA.	
ID	Q7M183	PRELIMINARY;	DR	GO; GO:0003700; F: transcription factor activity; IEA.
AC		RT	GO; GO:0006355; P: regulation of transcription, DNA-dependent; IEA.	
AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR0010982; Lambda like DNA.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR0010982; Lambda like DNA.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR0010982; Lambda like DNA.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR0010982; Lambda like DNA.		
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AC		InterPro; IPR001761; PeriplaBP/Laci.		
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AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
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AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR001761; PeriplaBP/Laci.		
AC		InterPro; IPR000843; HTH Laci.		
AC		InterPro; IPR0010982; Lambda like DNA.		
AC	</			

PRINTS; PR00036; HTHLACI.
DR SMART; SM00354; HTH_LACI; 1.
DR PROSITE; PS00356; HTH_LACI_1; 1.
DR PROSITE; PS00352; HTH_LACI_2; 1.
KW Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 333 AA; 36096 MW; 21D720P8696765F0 CRC64;
Query Match 63.5%; Score 40; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 IPVLDENGIFAP 12
Db : ||||| |
Db 253 LSVDENGILKVP 264

Search completed: January 7, 2005, 10:03:56
Job time : 111 secs

This frog drank (uspi~,